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L1 32100 SEA FILE=REGISTRY ABB=ON E...H/SQSP  
 L4 32000 SEA FILE=REGISTRY ABB=ON L1 ABB=ON L4=ON  
 L 32000 SEA FILE=REGISTRY ABB=ON L4 OR L4  
 L1 15000 SEA FILE=REGISTRY FAN= 159234-43-7, ABB=ON L4 OR L4  
 L4 17000 SEA FILE=REGISTRY ABB=ON L1 NOT L4  
 L 1140 SEA FILE=H'APLUS ABB=ON L6  
 L1 13900 SEA FILE=H'APLUS ABB=ON L7  
 L13 17800 SEA FILE=H'APLUS ABB=ON FATTY ACID#  
 L11 1200 SEA FILE=H'APLUS ABB=ON L11(GA)DESATUR?  
 L12 0 SEA FILE=H'APLUS ABB=ON (L1 OR L11 AND L11  
 L13 0 SEA FILE=H'APLUS ABB=ON L11 AND MUTANT  
 L14 0 SEA FILE=H'APLUS ABB=ON L11 AND DELTA(W (15 OR 12)  
 L11 210 SEA FILE=H'APLUS ABB=ON (L1 OR L11 AND L10  
 L16 0 SEA FILE=H'APLUS ABB=ON L11 AND MUTANT  
 L17 0 SEA FILE=H'APLUS ABB=ON L11 AND DELTA(W (15 OR 12)  
 L18 10 SEA FILE=H'APLUS ABB=ON L11 OR L14 OR L17  
 L11 0 SEA FILE=H'APLUS ABB=ON L11 AND MUTANT?  
 L12 0 SEA FILE=H'APLUS ABB=ON L11 AND MUTANT?  
 L13 0 SEA FILE=H'APLUS ABB=ON L21 AND DELTA(W (12 OR 15)  
 L14 10 SEA FILE=H'APLUS ABB=ON L11 OR L22 OR L23

=> d 124 1-19 bib abs ind

- 1997:628484 Document No. 107:316934 Rapid and transient induction of a parsley microsomal **.DELTA.12 fatty acid desaturase** mRNA by fungal elicitor. Kirsch, Christoph; Hahlbrock, Klaus; Schüssich, Imre E. (Max-Planck-Institut für Wirkstoffforschung, Abteilung Biochemie, Cologne, D-50929, Germany). Plant Physiol., 115(1), 283-289 (English) 1997. CODEN: PLPHAY. ISSN: 0032-0839. Publisher: American Society of Plant Physiologists.
- AB Treatment of cultured parsley (*Petroselinum crispum*) cells with a structurally defined peptide elicitor (Pep25) of fungal origin has previously been shown to cause rapid and large changes in the levels of various **desatd. fatty acids**. Two distinct parsley cDNAs were isolated sharing high sequence similarity with microsomal **omega-6 fatty acid desaturases** (FADs). One of them was functionally identified as a **.DELTA.12 FAD** by expression in the yeast *Saccharomyces cerevisiae*. Two diastolic fatty acids, hexadecadienoic and linoleic, which were not detectable in control cells, together constituted up to 1% of the total fatty acids in the transformed yeast cells. **.DELTA.12 FAD** mRNA accumulated rapidly and transiently in elicitor-treated parsley cells, protoplasts, and leaves. These and previous results indicate that **fatty acid desatn.** is an important early component of the complex defense response of parsley to attempted fungal infection.
- CC 11-1 (Plant Biochemistry)  
Section cross-reference(s): 3, 7
- ST parsley **fatty acid desaturase** fungal elicitor; infection fungi parsley **fatty acid desaturase**; Pep25 elicitor **fatty acid desaturase** parsley
- IT Phytoalexin-eliciting hormones  
EL: PAC (Biological activity or effector, except adverse); BIOL (Ecological study)  
(Pep25; rapid and transient induction of a parsley microsomal **.DELTA.12 fatty acid desaturase** mRNA by fungal elicitor)
- IT cDNA sequences  
(1c1 parsley microsomal **.DELTA.12 fatty acid desaturase** responsive to fungal elicitor)
- IT Protein sequences  
(1f parsley microsomal **.DELTA.12 fatty acid desaturase** responsive to fungal elicitor)
- IT Parsley (*Petroselinum crispum*)  
(rapid and transient induction of a parsley microsomal **.DELTA.12 fatty acid desaturase** mRNA by fungal elicitor)
- IT 197594-14-2 197594-15-3  
EL: BPP (Biological process); PRP (Properties); BIOL (Biological study); PPOC (Process)  
(omega acid sequence; rapid and transient induction of a parsley microsomal **.DELTA.12 fatty acid desaturase** mRNA by fungal elicitor)
- IT 15442-99-4, GenBank U70741 157698-97-3  
EL: BPP (Biological process); PRP (Properties); BIOL (Biological study); PPOC (Process)  
(nucleotide sequence; rapid and transient induction of a parsley microsomal **.DELTA.12 fatty acid desaturase** mRNA by fungal elicitor)
- IT 24628-1-9, Fatty acid **.DELTA.12-desaturase**  
EL: BPP (Biological process); PRP (Properties); BIOL (Biological study)  
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- study); PROC (Process)  
 (rapid and transient induction of a parsley microsomal  
 .DELTA.12 fatty acid  
 desaturase mRNA by fungal elicitor)
- IT 67826-35-4, Fatty acid .omega.-  
 desaturase  
 EL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
 (Biological study)  
 (rapid and transient induction of a parsley microsomal  
 .DELTA.12 fatty acid  
 desaturase mRNA by fungal elicitor)
- L24 ANSWER 2 OF 19 HCAPLUS COPYRIGHT 1997 ACS  
 1997:610711 Document No. 127:25444: The oleate desaturase product of  
 the FAD2-N gene of hazel and its uses. Dani, Maria; Catello, Sergio  
 (Spremaerts S.A., Belg.; Ferrero S.P.A.). Eur. Pat. Appl. EP 794250  
 A1 970910, 29 pp. DESIGNATED STATES: E: BE, ES, FR, GB, IT, NL.  
 (English). COCEN: EPXKDW. APPLICATION: EP 97-103023 970226.  
 PRIORITY: CH 97-150 260114.
- AB The FAD2-N gene of hazel (*Corylus avellana* L.) coding for the .  
 DELTA.12 desaturase enzyme of the microsomal  
 fraction is cloned and characterized for use as a probe for the  
 isolation of other plant desaturase genes. The gene can also be  
 used to alter the desaturase levels and consequently the  
 fatty-acid compn. of a plant. Probes derived from  
 the Arabidopsis .DELTA.12 desaturase gene were  
 used to screen a hazel cDNA bank from ripe *Corylus avellana* cv. San  
 Giovanni in .land-da.FAP11.
- IC 12M 01N 15-4;  
 12S 01N015-45; 012N02-02; 012N05-10; 012Q001-68
- ICA A01H005-00
- CC 7-2 (Enzymes)  
 Section cross-reference(s): 7, 11, 17
- ST Delta12 desaturase gene FAD2N Corylus; hazel delta12 desaturase gene  
 FAD2N
- IT Genes (plant)  
 EL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
 (Biological study)  
 (FAD2-N; oleate desaturase product of FAD2-N gene of hazel and  
 its uses)
- IT INA sequences  
 cDNA sequences  
 (cf. .DELTA.12 desaturase of hazel; oleate  
 desaturase product of FAD2-N gene of hazel and its uses)
- IT Fats and glyceric oils, Biological studies  
 EL: AGE (Agricultural use); BOC (Biological occurrence); FFD (Food  
 or feed use); BIOL (Biological study); OCCU (Occurrence); USES  
 (Uses)  
 (hazelnut, cloning of desaturase gene for altering  
 fatty acid profile of; oleate  
 desaturase product of FAD2-N gene of hazel and its uses)
- IT Fatty acids, biological studies  
 EL: AGE (Agricultural use); BOC (Biological occurrence); FFD (Food  
 or feed use); BIOL (Biological study); OCCU (Occurrence); USES  
 (Uses)  
 (cf hazel, cloning of desaturase gene for altering profile of;  
 oleate desaturase product of FAD2-N gene of hazel and its uses)
- IT Protein sequence  
 of .DELTA.12 desaturase of hazel; oleate  
 desaturase product of FAD2-N gene of hazel and its uses)
- IT Hazel (*Corylus avellana*)  
 oleate desaturase product of FAD2-N gene of hazel and its uses)
- IT Endoplasmic reticulum  
 (.DELTA.12 desaturase of hazelnut; oleate

desaturase product of FAD2-N gene of hazel and its uses)

IT 196217-78-4

EL: AGR (Agricultural use); BSU (Biological study, unclassified);  
PRP (Properties); BIOL (Biological study); USES (Uses)  
(amino acid sequence; oleate desaturase product of FAD2-N gene of  
hazel and its uses)

IT 196217-80-8

EL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
(Biological study)  
(amino acid sequence; oleate desaturase product of FAD2-N gene of  
hazel and its uses)

IT 196217-87-5 196217-78-5 196217-81-3

EL: AGR (Agricultural use); BSU (Biological study, unclassified);  
PRP (Properties); BIOL (Biological study); USES (Uses)  
(nucleotide sequence; oleate desaturase product of FAD2-N gene of  
hazel and its uses)

IT 59929-86-1, Oleate desaturase

EL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
(Biological study)  
(oleate desaturase product of FAD2-N gene of hazel and its uses)

L24 ANSWER 3 OF 19 HOAPLUS COPYRIGHT 1997 ACS

1997:51000 Document No. 127:13 124 Plants having mutant

sequences that confer altered **fatty acid**  
profiles. DeBonte, R. Lorin; Fan, Zhongang; Loh, H.-T. Willie  
(Cargill, Incorporated, USA; DeBonte, R. Lorin; Fan, Zhongang; Loh,  
H.-T. Willie). PCT Int. Appl. WO 9721440 A1 970619, 27 pp.  
INDICATED STATES: W: AL, AU, AT, AR, AU, BB, BG, BR, BY, CA, CH,  
CN, CU, DE, DK, EE, ES, FI, GB, GR, HU, IL, IN, JP, KE, KG, KP, KR,  
KZ, LA, LB, LG, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT,  
RU, SA, SD, SE, SG, SI, SK, TH, TM, TR, TT, UA, UG, US, VN, AM,  
AZ, BY, BG, BR, BS, BU, CH, CL, CN, CO, CR, CU, CY, CZ, DE, DK,  
DM, DO, DZ, EC, EE, EG, ES, FI, FR, GA, GB, GE, GR, GU, HK, HN, IL,  
IN, IS, IT, JP, KE, KG, KH, KR, KZ, LA, LB, LC, LG, LT, LU, LV, LY,  
MA, MC, MD, ME, MG, MK, MN, MU, MV, MW, MY, MZ, NA, NG, NI, NL,  
NU, NZ, OM, PA, PE, PG, PH, PK, PL, PT, QA, RO, RU, RW, SA, SD, SE,  
SG, SI, SK, SL, SM, SN, SR, ST, SV, SY, TD, TG, TH, TJ, TM, TN, TR,  
TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW. (English). COIN: PIXXD. APPLICATION: WO  
97-021199 961214. PRIORITY: US 95-17021 951214.

AB Seeds, plants and oils are provided having low FDA sats., high oleic  
acid, low linoleic acid,; high or low palmitic acid, low stearic  
acid, and low linoleic acid plus linolenic acid, and advantageous  
functional or nutritional properties. Plants are disclosed that  
contain a **mutation** in a **delta-12** or

**delta-15 fatty acid**

**desaturase** gene. Preferred plants are rapeseed and  
sunflower plants. Plants carrying such **mutant** genes have  
altered **fatty acid** compr. in seeds. In one  
embodiment, a plant contains a **mutation** in a region having  
the conserved motif His-Xaa-Xaa-Xaa-His, found in **delta-**  
**12 and delta-15 fatty**

**acid desaturases**. A preferred motif has the  
sequence His-Glu-Cys-Gly-His. A preferred **mutation** in  
this motif has the amino acid sequence His-Lys-Cys-Gly-His. Nucleic  
acid fragments are disclosed that comprise a **mutant**

**delta-12 or delta-15**

**fatty acid desaturase** gene sequence.

IC 101 A01H011-16

ICS A01H001-10; A01H011-40; C12N015-03; C07C037-02; C07C037-03;  
C07C033-126

CC 1-9 Food and Feed Chemistry)

Section cross-reference(s): 11

ST **fatty acid** profile alteration plant

**mutation**; Brassica **fatty acid** profile  
alteration **mutation**; Helianthus **fatty**  
**acid** profile alteration **mutation**

IT Pollination

(cross; plants having **mutant** sequences that confer altered **fatty acid** profiles)

IT Genes

PL: BAC (Biological activity or effector, except adverse); BIOL (Biological study)

(microsome; plants having **mutant** sequences that confer altered **fatty acid** profiles)

IT Brassica campestris

Brassica napus

Cruciferae (Brassicaceae)

Helianthus

Mitogenesis

**Mutation**

(plants having **mutant** sequences that confer altered **fatty acid** profiles)

IT **Fatty acids, biological studies**

PL: BOC (Biological occurrence); BPE (Biological process); BIOL (Biological study); OCCU (Occurrence); PROC (Process)

(plants having **mutant** sequences that confer altered **fatty acid** profiles)

IT Vegetable oils

PL: BOC (Biological occurrence); BEM (Removal or disposal); BIOL (Biological study); OCCU (Occurrence); PROC (Process)

(plants having **mutant** sequences that confer altered **fatty acid** profiles)

IT Cattle oil

PL: BPE (Biological process); BIOL (Biological study); PROC (Process)

(plants having **mutant** sequences that confer altered **fatty acid** profiles)

IT ~~12-10-3~~, Ethylmercaptosulfonate 71427-04-4, **.DELTA.**

**15-Fatty acid desaturase**

12536-78-8, **.DELTA.12-Fatty**

**acid desaturase** 192881-61-1 192881-62-6

192881-63-7 192881-64-8

PL: BAC (Biological activity or effector, except adverse); BIOL (Biological study)

(plants having **mutant** sequences that confer altered **fatty acid** profiles)

IT 192889-74-0 192889-75-1 192889-76-2 192889-77-3

192889-78-4 192889-79-5 192889-80-6 192889-81-9

PL: BAC (Biological activity or effector, except adverse); BPE (Biological process); BIOL (Biological study); PROC (Process)

(plants having **mutant** sequences that confer altered **fatty acid** profiles)

IT 12-10-3, Palmitic acid, biological studies 37-11-4, Stearic acid,

biological studies 40-13-3, Linoleic acid, biological studies

112-10-1, Oleic acid, biological studies 463-40-1,

alpha-linolenic acid 192823-14-4 192823-15-5 192823-16-6

192823-17-7 192823-18-8

PL: BOC (Biological occurrence); BIOL (Biological study); OCCU (Occurrence)

(plants having **mutant** sequences that confer altered **fatty acid** profiles)

L24 ANSWER 4 OF 1 - NCAPLUS COPYRIGHT 1997 AIS

1997: 11385 Document No. 126:233-96 Microbial and plant genes for **.DELTA.6-desaturases** and their use in increasing tissue levels of gamma-linolenic acid. Thomas, Terry L.; Reedy, Aratu S.; Nuccio, Michael; Nurnberg, Andrew W.; Freyssinet, Georges L. (Rhône-Poulenc Agrochimie, Fr.). U.S. 5614391 A 970325, 30 pp. Cont.-in-part of U.S. 5,582,596. (English). CODEN: USKKAM. APPLICATION: US 94-366779 941230. PRIORITY: US 91-324475 911010; US 92-817919 920108; US 92-959952 921013; US 94-307382 940914.

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- AB Microbial genes for .DELTA.6-desaturases are cloned and characterized for use in the prepn. of transgenic organisms synthesizing high levels of .gamma.-linolenic acid from linoleic acid. Plants expressing a desaturase gene and with high tissue levels of .gamma.-linolenic acid are chilling resistant. These plants can also be used to produce oils with altered levels .gamma.-linolenic acid. The Synechocystis .DELTA.6-desaturase was cloned by expression in a .gamma.-linolenate-deficient Anabena. Expression of the gene in transgenic tobacco and carrot is demonstrated.
- IC ICM 12N013-83  
IC 12N013-82; C12N011-81; C12P007-84
- NCL 439134006
- CC 7-1. (Enzymes)
- ST delta: desaturase gene Synechocystis borage; gamma linolenate manuf  
delta: desaturase
- IT Plasmid vectors  
(1.1.DELTA.6NOS, borage .DELTA.6-desaturase gene on, expression in carrot cell culture and tobacco of; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT Plasmid vectors  
(2.1.DELTA.6NOS, borage .DELTA.6-desaturase gene on, expression in carrot cell culture and tobacco of; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT Carrot  
(cell cultures as expression host; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT Corn  
Filamentous fungi  
Pearl  
Rape (plant)  
Soybean  
Sunflower  
Tobacco  
(expression host; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT Anabena  
(expression of .DELTA.6-desaturase genes from carboxylase promoter of; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT Glycins  
EL: MSC (Miscellaneous)  
(expression of .DELTA.6-desaturase genes from promoter of gene for; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT 35S promoter (genetic element)  
EL: BTU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(expression of .DELTA.6-desaturase genes from; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT DNA sequences  
(for .DELTA.6-desaturase of Synechocystis; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT cDNA sequences  
(for .DELTA.6-desaturase of borage; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)

- IT Genes (microbial)  
Genes (plant)  
EL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)  
(for .DELTA.6-desaturase, cloning and -expression of; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT Globulins, miscellaneous  
EL: MSC (Miscellaneous)  
(helianthins, expression of .DELTA.6-desaturase genes from promoter of gene for; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT Globulins, miscellaneous  
EL: MSC (Miscellaneous)  
(helianthins, expression of .DELTA.6-desaturase genes from promoter of gene for; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT Promoter (genetic element)  
EL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(homologous and heterologous, expression of .DELTA.6-desaturase genes from; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT Albumins, miscellaneous  
EL: MSC (Miscellaneous)  
(napins, expression of .DELTA.6-desaturase genes from promoter of gene for; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT Protein sequences  
(of .DELTA.6-desaturases of *Synechocystis* and borage; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT Cold stress (plant)  
(transgenic plants resistant to; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT Borage officinalis  
*Synechocystis*  
(.DELTA.6-desaturase gene of; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT **148734-39-8 180583-92-0, Desaturase, linoleate**  
(*Borago officinalis*)  
EL: AGE (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)  
(amino acid sequence; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT 9051-31-4, Carboxylase  
EL: MSC (Miscellaneous)  
(expression of .DELTA.6-desaturase genes from *Anabena* promoter of gene for; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT 7142-04-8, **.DELTA.15-Desaturase**  
8462-21-8  
EL: AGE (Agricultural use); BPN (Biosynthetic preparation); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)  
(gene for, in engineering **fatty acid** profiles; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)

- IT 91275-16-9P, octadecatetraenoic acid  
 RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)  
 (manuf. with transgenic microorganisms, .DELTA.6-desaturase genes in; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT 992-26-0P, .DELTA.6-Desaturase  
 RL: AGE (Agricultural use); BPN (Biosynthetic preparation); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)  
 (microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT 438-48-1, .alpha.-Linolenic acid  
 RL: BPN (Biological study, unclassified); BIOL (Biological study)  
 (microorganisms producing, manuf. of .gamma.-linolenate with; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT 19033-81-1 19033-81-2 19033-81-3  
 RL: AGE (Agricultural use); BPN (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)  
 (nucleotide sequence; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT 508-26-1P, .gamma.-Linolenic acid  
 RL: AGE (Agricultural use); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation); USES (Uses)  
 (prepn. from linoleic acid of; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)
- IT 508-26-1, 9,12-Octadecadienoic acid (C, Z -, reactions  
 RL: BPN (Reagent)  
 (.gamma.-linolenic acid prepn. from; microbial and plant genes for .DELTA.6-desaturases and their use in increasing tissue levels of .gamma.-linolenic acid)

L24 ANSWER 5 OF 15 HEADLINE COPYRIGHT 1997 ACS

1997: 12341 Document No. 126: 95447 Temperature-regulated mRNA accumulation and stabilization for **fatty acid desaturase** genes in the cyanobacterium *Synechococcus* sp. strain PCC 7102. Sakamoto, Tetsuo; Bryant, Donald A. (Department of Biochemistry and Molecular Biology, The Pennsylvania State University, University Park, PA, 16802, USA). Mol. Microbiol., 1997, 1261-1268 (English) 1997. CODEN: MICROE. ISSN: 0950-4230. Publisher: Blackwell.

AB Cyanobacteria adaptate to low-temp. conditions by desaturating their membrane lipids. The *desB* (omega-3 desaturase) and *desC* (.DELTA.12 desaturase) genes of *Synechococcus* sp. strain PCC 7102 were cloned and characterized, and the expression of the *desA* (.DELTA.12 desaturase), *desB* and *desC* genes was studied as a function of temp. The steady-state mRNA abundance for the *desA* gene was threefold higher in cells grown at 22.degree.C than in cells grown at 38.degree.C. *DesB* transcripts were not detected at 38.degree.C, but were abundant in cells grown at 22.degree.C. Levels of *desC* mRNA were similar at both growth temps. The mRNA levels of each desaturase gene increased within 15 min of a temp. shift-down to 22.degree.C, and mRNA level recovered within 15 min after a shift-up to 38.degree.C. The cold-induced accumulation of transcripts from the *desA* and *desB* genes was suppressed by the addn. of chloramphenicol, but the transient elevation of the *desC* transcript levels at 22.degree.C was not affected by chloramphenicol. The half-lives of the *desA* and *desB* mRNAs were significantly longer in cells grown at 22.degree.C than in cells grown at 38.degree.C, but the *desC* mRNA had a similar half-life at both temps. These studies reveal three patterns of temp. regulation

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for the desaturase genes, whose expression is tightly controlled by a combination of mRNA synthesis and stabilization. These studies demonstrate that elevation of desaturase mRNA levels is not the rate-limiting event during the low-temp. acclimation of cyanobacteria.

- CC 1F-1 (Microbial, Algal, and Fungal Biochemistry)  
Section cross-reference(s): \*
- ST Synchococcus **fatty acid desaturase**  
gene sequence
- IT Genes (microbial)  
EL: FFP (Properties)  
Desat; temp.-regulated mRNA accumulation and stabilization for **fatty acid desaturase** genes in  
Cyanobacterium Synchococcus sp. strain PCC 7002
- IT Genes (microbial)  
EL: FFP (Properties)  
Desat; temp.-regulated mRNA accumulation and stabilization for **fatty acid desaturase** genes in  
Cyanobacterium Synchococcus sp. strain PCC 7002
- IT Genes (microbial)  
EL: FFP (Properties)  
Desat; temp.-regulated mRNA accumulation and stabilization for **fatty acid desaturase** genes in  
Cyanobacterium Synchococcus sp. strain PCC 7002
- IT DNA sequences  
Protein sequences  
Synchococcus  
Temperature effects (biological)  
temp.-regulated mRNA accumulation and stabilization for **fatty acid desaturase** genes in  
Cyanobacterium Synchococcus sp. strain PCC 7002
- IT mRNA  
EL: FFP (Properties)  
temp.-regulated mRNA accumulation and stabilization for **fatty acid desaturase** genes in  
Cyanobacterium Synchococcus sp. strain PCC 7002
- IT 156532-36-4  
EL: FFP (Properties)  
Fatty acid sequence; temp.-regulated mRNA accumulation and stabilization for **fatty acid desaturase** genes in Cyanobacterium Synchococcus sp. strain PCC 7002
- IT 156403-aa-1, GenBank D03773 189176-aa-2, GenBank U36389  
189176-aa-3, GenBank U36391  
EL: FFP (Properties)  
Nucleotide sequence; temp.-regulated mRNA accumulation and stabilization for **fatty acid desaturase** genes in Cyanobacterium Synchococcus sp. strain PCC 7002
- IT 2014-34-6, **Fatty acid desaturase**  
EL: FFP (Properties)  
temp.-regulated mRNA accumulation and stabilization for **fatty acid desaturase** genes in  
Cyanobacterium Synchococcus sp. strain PCC 7002

L24 ANSWER 6 OF 19 NCAPLUN COPYRIGHT 1997 ACS  
1996:7 9:9 Document No. 126:113911 The P-OLE1 gene of *Pichia angusta* encodes a **DELTA-9-fatty acid desaturase** and complements the ole1 mutation of *Saccharomyces cerevisiae*. Aramant, Sarinip; Tomita, Tetsushi; Fukui, Fumio; Fujimori, Ko; Harashima, Satoshi; Yamada, Yasuhiro; Oshima, Yasuji (Department of Biotechnology, Faculty of Engineering, Osaka University, 2-1 Yamadaoka, Suita-shi, Osaka, 565, Japan). Gene, 164(2), 293-306 (English) 1997. CODEN: GENED6. ISSN: 0378-1119.

Publisher: Elsevier.

AB Three PCR-amplified DNA fragments hybridizing with the OLE1 gene encoding **.DELTA.9-fatty acid desaturase** of *Saccharomyces cerevisiae* were obtained using, resp., genomic DNAs of one strain each of *Kluyveromyces thermotolerans*, *Pichia angusta* and *Yarrowia lipolytica* as templates. A gene designated P-OLE1 was cloned from the above fragment of *P. angusta* and sequenced. An open reading frame of P-OLE1 encodes a 49.6-kDa protein consisting of 451 amino acid residues, which shows high identity (62) and similarity (19) to that deduced from the OLE1 nucleotide sequence. Expression of P-OLE1 driven by the *S. cerevisiae* GAP promoter or its own promoter complemented the ole1 **mutation** of *S. cerevisiae*. Transcription of P-OLE1 in the native host was suggested to be partially repressed by oleic acid in the medium, as was that of OLE1 in *S. cerevisiae* and a similar gene in *Y. lipolytica*, but that of a similar gene in *K. thermotolerans* was not.

CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 7, 10

ST P-OLE1 gene **fatty acid desaturase**  
sequence; *Pichia* **fatty acid desaturase**  
gene sequence

IT Genes (microbial)

EL: ANT (Analyte); BPA (Biological process); BPP (Properties); ANST (Analytical study); BIOL (Biological study); PPOC (Process)  
(P-OLE1; the P-OLE1 gene of *Pichia angusta* encodes a **.DELTA.9-fatty acid desaturase** and complements the ole1 **mutation** of *Saccharomyces cerevisiae*)

IT Protein sequences

(of *Pichia angusta* **.DELTA.9-fatty acid desaturase** 7)

IT DNA sequences

(of the P-OLE1 gene of *Pichia angusta* encoding a **.DELTA.9-fatty acid desaturase** and complementing the ole1 **mutation** of *Saccharomyces cerevisiae*)

IT *Pichia angusta*

*Saccharomyces cerevisiae*

(the P-OLE1 gene of *Pichia angusta* encodes a **.DELTA.9-fatty acid desaturase** and complements the ole1 **mutation** of *Saccharomyces cerevisiae*)

IT 102-35-1, Oleic acid, biological studies

EL: BAC (Biological activity or effector, except adverse); BIOL (Biological study)

(P-OLE1 gene of *Pichia angusta* encoding a **.DELTA.9-fatty acid desaturase** and complementing the ole1 **mutation** of *Saccharomyces cerevisiae* repressed by oleic acid)

IT 186208-06-0

EL: BAC (Biological activity or effector, except adverse); BPP (Properties); BIOL (Biological study)

(Oleic acid sequence; the P-OLE1 gene of *Pichia angusta* encodes a **.DELTA.9-fatty acid desaturase** and complements the ole1 **mutation** of *Saccharomyces cerevisiae*)

IT 186209-16-5

EL: BPP (Properties)

(nucleotide sequence; the P-OLE1 gene of *Pichia angusta* encodes a **.DELTA.9-fatty acid desaturase** and complements the ole1 **mutation** of *Saccharomyces cerevisiae*)

IT P014-64-0, **.DELTA.9-Fatty acid desaturase**

EL: BAC (Biological activity or effector, except adverse); BPP (Properties); BIOL (Biological study)

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(the P-OLE1 gene of *Pichia angusta* encodes a .DELTA.9-  
fatty acid desaturase and complements  
the ole1 mutation of *Saccharomyces cerevisiae*)

L24 ANSWER 7 OF 13 NCAPLUS COPYRIGHT 1997 ACS

1996:239644 Document No. 124:319.85 Isolation and characterization of an *Arabidopsis thaliana* cDNA encoding a .DELTA.7-sterol-C-5-desaturase by functional complementation of a defective yeast mutant. Gascotte, Daniel; Hasselstein, Tania; Bard, Martin; Lacroix, Francois; Benveniste, Pierre (Department de Biologie Cellulaire et Moleculaire, Institut de Botanique, Strasbourg, 67083, Fr.). Plant J., 9(3), 291-9 (English) 1996. CODEN: PLJED. ISSN: 0950-7412.

AB A yeast null mutant (*erg3*) defective in EFG 3, the gene encoding the C-5 sterol desaturase required for ergosterol synthesis was transformed with an *Arabidopsis thaliana* cDNA library inserted in a yeast vector. Transformants (4.times.10<sup>5</sup>) were screened for cycloheximide (CH) resistance and 400 possible clones were analyzed to det. their sterol profile. Low levels of ergosterol in addn. to .DELTA.7- and .DELTA.8-sterols normally present in *erg3* were isolated in three yeast transformants. Characterization of one transformant indicated a cDNA of 1141 bp. Transformation of an *erg3* strain with this plasmid led to CH resistance, nystatin sensitivity and an ergosterol profile. After sub-cloning in a pBlueScript vector and subsequent sequencing, an ORF of 543 bp encoding a possible 291 amino acid polypeptide was deduced. Three histidine-rich motifs (HX<sub>1</sub>H, HX<sub>2</sub>HH and HX<sub>3</sub>HH) were found in the *A. thaliana* ORF which are also present in the yeast EFG 3 gene. These histidine-rich motifs are also characteristic of many membrane-bound fatty acid desaturases from higher plants. These data strongly suggest that the *A. thaliana* cDNA encodes a .DELTA.7-sterol-C-5-desaturase.

CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 7, 11

ST *Arabidopsis* sterol desaturase cDNA sequence gene

IT Gene, plant

RL: PPP (Properties)

After C-5 sterol desaturase; isolation and characterization of *Arabidopsis thaliana* cDNA encoding .DELTA.7-sterol-C-5-desaturase by functional complementation of defective yeast mutant

IT *Arabidopsis thaliana*

Protein sequences

Isolation and characterization of *Arabidopsis thaliana* cDNA encoding .DELTA.7-sterol-C-5-desaturase by functional complementation of defective yeast mutant.

IT Deoxyribonucleic acid sequences

Complementary, isolation and characterization of *Arabidopsis thaliana* cDNA encoding .DELTA.7-sterol-C-5-desaturase by functional complementation of defective yeast mutant

IT 175960-67-5

RL: PPP (Properties)

Amino acid sequence contg. three histidine-rich motifs; isolation and characterization of *Arabidopsis thaliana* cDNA encoding .DELTA.7-sterol-C-5-desaturase by functional complementation of defective yeast mutant

IT 37215-37-1

RL: BUU (Biological use, unclassified); BIOI (Biological study); USES (Uses)

Isolation and characterization of *Arabidopsis thaliana* cDNA encoding .DELTA.7-sterol-C-5-desaturase by functional complementation of defective yeast mutant

IT 170611-11-7, Genbank X90454

RL: PPP (Properties)

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(nucleotide sequence; isolation and characterization of *Arabidopsis thaliana* cDNA encoding .DELTA.7-sterol-C-6-desaturase by functional complementation of defective yeast mutant

L24 ANSWER 3 OF 19 HCAPLUS COPYRIGHT 1997 ACS

1995:235095 Document No. 127:50097 Molecular cloning of cDNA for

**fatty acid desaturase** of *Anacyctis*

*nidulans* and its use in creating transgenic plant resistant to cold temperature. Nishizawa, Osamu; Toguri, Toshihiro (Kirin Beer K. K., Japan). PCT Int. Appl. WO 94/22221 A1 090106, 41 pp. DESIGNATED

STATES: W: AM, AU, BB, BG, BR, BY, CA, CN, CZ, FI, GE, HU, JP, KG, KR, KZ, LK, LU, LV, MD, MG, MN, NO, NL, PL, RO, RU, SI, SK, TH, TT, UA, US, UZ, VN; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB, GR, IE, IT, LB, LI, MC, ML, ME, NE, NL, PT, SE, SN, TD, TG. (Japanese). CODEN: PINKD2. APPLICATION: WO 94-JP22221 941223.

PRIORITY: JP 8-350853 931223.

AB Gene des 9 var fragment of *Anabaena variabilis* IAM N-3 is isolated upstream from gene desA that encodes .DELTA.-12

unsaturase and used as a probe for the isolation of open reading frame (ORF) des 9 mid of *Anacyctis nidulans*. ORF des 9 mid codes for a desaturase desaturating the .DELTA.-position of a fatty acid bound to a lipid and exhibits 80 and 80% similarity to gene des 9 var of *Anabaena variabilis* and stearoyl-CoA unsaturase of mouse, resp. The ORF introduced into transgenic tobacco plants increased the content of unsatd. fatty acids and the resistance to cold temp.

IC ICH GEN-11-44

IC3 GEN-03-44; AG1H04-11; AG1H03-10

ICA CLINT03-0

CC 7-2 (Enzymes)

Section cross-reference(s): 1.

ST *Anacyctis* **fatty acid desaturase** cDNA

sequence; cold resistance des 9 mid *Anacyctis*; transgenic plant unsatd fatty acid

IT Gene, plant

EL: AGE (Agricultural use); P&P (Properties); BIOL (Biological study); USES (Uses).

des 9 mid; cloning of cDNA for .DELTA.9-fatty acid desaturase of *Anacyctis nidulans* and its use in creating transgenic plant resistant to cold temp.)

IT Protein sequences

of .DELTA.9-fatty acid desaturase of *Anacyctis nidulans*

IT Plant cell

Plant

Tobacco

transgenic; expression of cDNA for .DELTA.9-fatty acid desaturase of *Anacyctis nidulans* in

IT Temperature effects, biological

cold; expression of cDNA for .DELTA.9-fatty acid desaturase of *Anacyctis nidulans* in transgenic plants to increase resistance to

IT Deoxyribonucleic acid sequences

complementary, for .DELTA.9-fatty acid desaturase of *Anacyctis nidulans*

IT Fatty acids, miscellaneous

EL: MSC (Miscellaneous)

consist., expression of cDNA for .DELTA.9-fatty acid desaturase of *Anacyctis nidulans* in transgenic plants to increase content of

IT 168613-13-6

EL: AGE (Agricultural use); P&P (Properties); BIOL (Biological study); USES (Uses).

(amino acid sequence; cloning of cDNA for .DELTA.9-fatty

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- acid desaturase** of *Anacystis nidulans* and its use in creating transgenic plant resistant to cold temp.)
- IT 166922-04-3  
 PL: AGE (Agricultural use); PPE (Properties); BIOL (Biological study); USES (Uses)  
 (nucleotide sequence; cloning of cDNA for **.DELTA.9-fatty acid desaturase** of *Anacystis nidulans* and its use in creating transgenic plant resistant to cold temp.)
- L24 ANSWER 1 OF 13 RTAPLUS COPYRIGHT 1997 ACS  
 1995:27-449 Document No. 12:26803 Identification of a gene that complements an *Arabidopsis* **mutant** deficient in chloroplast **.omega.6** desaturase activity. Falcone, Peane L.; Gibson, Susan; Lemieux, Bertrand; Somerville, Chris (Dep. Plant Biol., Carnegie Inst., Stanford, CA, 94305, USA). *Plant Physiol.*, 107(4), 1453-9 (English) 12-4. CODEN: PLPHAY. ISSN: 0032-0859.
- AB Membrane lipids of the **fad6** (formerly **fadC**) **mutant** of *Arabidopsis*, which is deficient in chloroplast **.omega.6** desaturase activity, have increased levels of monounsaturated **fatty acids** and are deficient in trienoic **fatty acids**. A putative **fad6** cDNA clone was isolated by probing a cDNA library with a degenerate oligonucleotide based on a conserved region within known **.omega.3** desaturase genes. Expression of the cDNA in transgenic plants of a **fad6 mutant** restored normal levels of all **fatty acids**. When used as a hybridization probe, the cDNA identified a restriction fragment-length polymorphism that co-segregated with the **fad6 mutation**. Thus, on the basis of a genetic complementation test and genetic map position, the **fad6** gene is encoded by the cDNA. The cDNA encoded a 418-amino acid polypeptide of 47,725 that displayed a high degree of sequence similarity to a **.DELTA.12** desaturase from the cyanobacterium *Synechocystis*. The **fad6** gene exhibited less sequence homol. to any known higher plant desaturase, including an endoplasmic reticulum-located **.omega.6** desaturase corresponding to the *Arabidopsis* **fad2** gene.
- CC 7-8 Enzymes.  
 Section cross-reference(s): 3, 11
- ST **fatty acid .omega.6 desaturase** sequence  
*Arabidopsis*; cDNA **.omega.6** desaturase sequence *Arabidopsis* chloroplast; gene **fad6** sequence **.omega.6** desaturase *Arabidopsis*
- IT Gene, plant  
 EL: PEP (Properties)  
 (clon; identification of gene that complements *Arabidopsis* **mutant** deficient in chloroplast **.omega.6** desaturase activity)
- IT *Arabidopsis thaliana*  
 Chloroplast  
 Leaf  
 Protein sequence  
 (identification of gene that complements *Arabidopsis* **mutant** deficient in chloroplast **.omega.6** desaturase activity)
- IT **Fatty acids**, biological studies  
 EL: BOC (Biological occurrence); NFM (Metabolic formation); BIOL (Biological study); FERM (Formation, nonpreparative); OCCU (Occurrence)  
 (identification of gene that complements *Arabidopsis* **mutant** deficient in chloroplast **.omega.6** desaturase activity)
- IT Deoxyribonucleic acid sequences  
 (complementary, identification of gene that complements *Arabidopsis* **mutant** deficient in chloroplast **.omega.6** desaturase activity)
- IT 163961-98-6

PL: BAC (Biological activity or effector, except adverse); PRP (Properties); BIOL (Biological study)  
 (identification of gene that complements Arabidopsis mutant deficient in chloroplast .omega.6 desaturase activity)

IT 06823-01-4, **Fatty acid .omega.6-Desaturase**

PL: BOC (Biological occurrence); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); OCCU (Occurrence)

(identification of gene that complements Arabidopsis mutant deficient in chloroplast .omega.6 desaturase activity)

IT 15573-04-0, GenBank U19 93

PL: PRP (Properties)

nucleotide sequence of; identification of gene that complements Arabidopsis mutant deficient in chloroplast .omega.6 desaturase activity)

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1995:176174 Document No. 127:174842 Cloning of .omega.3 desaturase from cyanobacteria and its use in altering the degree of membrane-lipid unsaturation. Sakamoto, Toshio; Lis, Dmitry A.; Higashi, Shoichi; Wada, Harumi; Nishida, Ikko; Onmori, Masayuki; Murate, Hario (Department Molecular Biomechanics, Graduate University Advanced Studies, Okazaki, 444, Japan). Plant Mol. Biol., 20(1), 249-57 (English) 1994. CODEN: PHEIIB. ISSN: 0167-4411.

AB Cyanobacteria respond to a decrease in temp. by **desaturating fatty acids** of membrane lipids to compensate for the decrease in membrane fluidity. Among various desatn. reactions in cyanobacteria, the desatn. of the .omega.3 position of **fatty acids** is the most sensitive to the change in temp. In the present study, the authors isolated a gene, designated *desB*, for the .omega.3 desaturase from the cyanobacterium, *Synechocystis* sp. PCC 6803. The *desB* gene encodes a protein a 359 amino-acid residue with mol. mass of 41.7 kDa. The *desB* gene is transcribed as a monocistronic operon that produced a single transcript of 1.4 kb. The level of the *desB* transcript in cells grown at 17.degree. was 10-times higher than that in cells grown at 24.degree.. To manipulate the **fatty-acid** unsatn. of membrane lipids, the *desB* gene in *Synechocystis* sp. PCC 6803 was **mutated** by insertion of a kanamycin-resistance gene cassette. The resultant **mutant** was unable to **desaturate fatty acids** at the .omega.3 position. The *desA* gene, which encodes the .DELTA.12 desaturase of *Synechocystis* sp. PCC 6803, and the *desB* gene were introduced into *Synechococcus* sp. PCC 7942. While the parent cyanobacterium can only desaturate membrane lipids at the .DELTA.9 position of **fatty acids**, the resultant transformant was able to **desaturate fatty acids** of membrane lipids at the .DELTA.9, .DELTA.12 and .omega.3 positions. These results confirm the function of the *desB* gene and demonstrate that it is possible to genetically manipulate the **fatty-acid** unsatn. of membrane lipids in cyanobacteria.

CC 3-3 (Biochemical Genetics)

Section cross-reference 1): 7, 10

ST cloning sequence omega3 desaturase gene Synechocystis; Synechocystis desaturase alteration membrane lipid unsatn; gene desB sequence omega3 desaturase Synechocystis; transcription omega3 desaturase gene Synechocystis temp; desaturase delta12 omega3 Synechocystis transformation Synechococcus

IT Synechococcus

- Transformation, genetic  
 (alteration of membrane lipid unsatn. in *Synechococcus* sp. PCC 7941 by transformation with  $\omega$ -3- and **.DELTA**.  
**12** desaturase genes from *Synechocystis* sp. PCC 6813)
- IT Lipids, biological studies  
 RL: MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)  
 (alteration of membrane lipid unsatn. in *Synechococcus* sp. PCC 7941 by transformation with  $\omega$ -3- and **.DELTA**.  
**12** desaturase genes from *Synechocystis* sp. PCC 6813)
- IT **Fatty acids**, biological studies  
 RL: MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)  
 (changes in **fatty acid** compn. of total lipids upon transformation of *Synechococcus* sp. PCC 7942 with  $\omega$ -3- and **.DELTA.12** desaturase genes from *Synechocystis* sp. PCC 6813)
- IT *Synechocystis*  
 (cloning and sequence of  $\omega$ -3 desaturase from *Synechococcus* and its use in altering the degree of membrane-lipid unsatn.)
- IT Cell membrane  
 Deoxyribonucleic acid sequences  
 Protein sequences  
 (cloning and sequence of  $\omega$ -3 desaturase from *Synechocystis* and its use in altering the degree of membrane-lipid unsatn.)
- IT Cyanobacteria  
 (cloning and sequence of  $\omega$ -3 desaturase from cyanobacteria and its use in altering the degree of membrane-lipid unsatn.)
- IT Gene, microbial  
 RL: BPF (Biological process); BPS (Properties); BIOL (Biological study); PROC (Process)  
 (desB; cloning and sequence of  $\omega$ -3 desaturase gene desB from *Synechococcus* and its use in altering the degree of membrane-lipid unsatn.)
- IT Temperature effects, biological  
 (temp. regulation of  $\omega$ -3 desaturase gene desB transcript levels in *Synechocystis*)
- IT Ribonucleic acids, messenger  
 RL: MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)  
 (temp. regulation of  $\omega$ -3 desaturase gene desB transcript levels in *Synechocystis*)
- IT Gene, microbial  
 RL: BPF (Biological process); BIOL (Biological study); PROC (Process)  
 (desA, **.DELTA.12** desaturase; alteration of membrane lipid unsatn. in *Synechococcus* sp. PCC 7941 by transformation with  $\omega$ -3- and **.DELTA.12** desaturase genes from *Synechocystis* sp. PCC 6813)
- IT 1213-45-1, **.DELTA.12** Desaturase  
 RL: BAC (Biological activity or effector, except adverse); BIOL (Biological study)  
 (alteration of membrane lipid unsatn. in *Synechococcus* sp. PCC 7941 by transformation with  $\omega$ -3- and **.DELTA**.  
**12** desaturase genes from *Synechocystis* sp. PCC 6813)
- IT 17-1-3, Hexadecadienoic acid, biological studies 37-11-4, C 18:0, biological studies 43-63-4, 9,11-Octadecadienoic acid (Z,Z)-, biological studies 113-60-1, 9-Octadecenoic acid (Z)-, biological studies 373-49-4, 9-Hexadecenoic acid, (Z)- 465-40-1 506-17-2, 11-Hexadecenoic acid (Z)- 5070-15-1, 9,11-Hexadecadienoic acid, Z,Z- 28-34-77-2, Octadecadienoic acid (Z,Z)- 323-9-14-0  
 RL: BOC (Biological occurrence); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); OCC (Occurrence)

(changes in **fatty acid** compn. of total lipids upon transformation of *Synechococcus* sp. PCC 7942 with  $\omega$ -3- and **.DELTA.12** desaturase genes from *Synechocystis* sp. PCC 6803)

IT 71427-24-3, **.DELTA.15** Desaturase  
161027-24-3

EL: EAC (Biological activity or effector, except adverse); PRP (Properties); BIOL (Biological study)  
(cloning and sequence of  $\omega$ -3 desaturase from cyanobacteria and its use in altering the degree of membrane-lipid unsat.)

IT 160234-15-7

EL: PRP (Biological process); PRP (Properties); BIOL (Biological study); PROC (Process)  
(cloning and sequence of  $\omega$ -3 desaturase from cyanobacteria and its use in altering the degree of membrane-lipid unsat.)

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1994:037899 Document No. 121:037899 Altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase. Gibson, Susan Irma; Kishore, Sanesh Murthy; Ruff, Thomas Gene; Somerville, Christopher Roland; Aronel, Vincent Jean-Marie Arnel Monsanto Co., USA; Michigan State University). IOT Int. Appl. WO 94/1337 A1 940318, 143 pp. DESIGNATED STATES: W: CA, GB, DE, ES; EW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, NL, PT, SE. (English). CODEN: PIXXD2. APPLICATION: WO 94-US1321 941204. PRIORITY: US 93-14431 930205; US 93-14431 931122.

AB The linolenic acid content of vegetable oils is altered by changing the levels of expression of linoleic acid desaturase, e.g. by expression of a heterologous gene or antisense gene for the enzyme. A cDNA for the enzyme derived from the *fad3* gene of *Brassica napus* was introduced into wild-type and *fad3* **mutants** of *Arabidopsis thaliana* by *Agrobacterium*-mediated transformation and transgenic plants prepd. Transformation of the wild type increased the linolenate content from 31.3 $\pm$ 4.3 to 31.3 $\pm$ 10.3 mol% of **fatty acids** and in the *fad3* **mutants** the increase was from 6.7 $\pm$ 1.7 to 43.1 $\pm$ 13.5 mol% of **fatty acids**.

ICM C12N15-34

ICS C12N 15-58; C12N017-11; C12N101-11; A01H003-11; C11B101-00

CC 11-1 Plant Biochemistry

Section cross-reference : 3

ST linoleate desaturase plant linoleic acid level

IT *Arabidopsis thaliana*

(*fad3* gene of; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)

IT Gene, plant

EL: BIOL (Biological study)

(*fad3*, for linoleate desaturase of *Brassica napus*; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)

IT Gene, plant

EL: BIOL (Biological study)

(*fad3*, of *Arabidopsis thaliana*; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)

IT Gene, plant

EL: BIOL (Biological study)

(*fad3*, for linoleate desaturase of *Arabidopsis thaliana*; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)

IT Gene, plant

EL: BIOL (Biological study)

(*fad3*, for linoleate desaturase of *Arabidopsis thaliana*; altering

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- the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase
- IT Protein sequences  
(of linoleic acid desaturases of Arabidopsis and Brassica)
- IT Plasmid and Episome  
(pMON13901, pMON13903, expression vectors for plants; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT Plasmid and Episome  
(pMON13904, pMON13905, Brassica napus linoleate desaturase antisense gene on; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT Plasmid and Episome  
(pTIDE33, Brassica napus linoleate desaturase gene on; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT Plasmid and Episome  
(pTIDE33, linoleate desaturase gene of Arabidopsis thaliana on; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT Plant  
Pape (plant)  
Seed  
Soybean  
(transgenic; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT Plant stress  
(cold, improved resistance to; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT Deoxyribonucleic acid sequences  
(complementary, for linoleic acid desaturases of Arabidopsis and Brassica)
- IT Deoxyribonucleic acids  
FL: BVT (Biological use, unclassified); BIOL (Biological study);  
USES (Uses)  
(complementary, antisense, to fad3 gene for linoleate desaturase of Arabidopsis thaliana; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT Microorganism  
(phytopathogenic, improved resistance to; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT Fats and Glyceridic oils  
FL: PME (Microindustrial manufacture); PRP (Properties); BIOL (Biological study); PREP (Preparation)  
(vegetable, altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT 112-41-1, 9-Octadecenoic acid (Z)-, biological studies 463-49-1, Linolenic acid 9052-06-0, Linoleic acid desaturase  
FL: AGE (Agricultural use); MEM (Metabolism formation); BIOL (Biological study); FORM (Formation, nonpreparative); USES (Uses)  
(altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT 148814-49-7 149955-97-5 158651-91-3  
FL: AGE (Agricultural use); PRP (Properties); BIOL (Biological study); USES (Uses)  
(amino acid sequence; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)
- IT T1427-(4-8), DELTA.15 Desaturase  
FL: AGE (Agricultural use); BOC (Biological occurrence); PRP

(Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses).

cloning of Arabidopsis thaliana gene for; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)

IT 13031-34-9 139203-33-0 11903-33-1

EL: AAF (Agricultural use); PRP (Properties); BIOL (Biological study); USES (Uses).

nucleotide sequence; altering the linolenic and linoleic acid content of plant oils by altering the levels of linoleic acid desaturase)

L24 ANSWER 12 OF 19 HCAELUS COPYRIGHT 1997 ACS

1994:226646 Document No. 131:226646 Molecular cloning of cDNA for microbial **delta-12 fatty acid**

**desaturases** and their use for molecular breeding of plants.

Lightner, Jonathan Edward; Oculley, John Joseph (du Pont de Nemours, E. I., ~~and Co.~~, USA; PCT Int. Appl. WO 941516 A1 340396, 147 pp.

DESIGNATED STATES: W: AU, BR, CA, CH, DE, ES, FR, GB, GR, IE, IT, LU, NL, PT, SE. (English). CODEN: EINDEX. APPLICATION: WO 94-22907 941013. PRIORITY: US 92-977339 921117.

AB The prepn. and use of nucleic acid fragments encoding **fatty**

**acid desaturases** and related enzymes are described. The invention permits alteration of plant lipid compn.

Chimeric genes incorporating such nucleic acid fragments with suitable regulatory sequences may be used to create transgenic plants with altered levels of unsatd. fatty acids. The cloning of cDNA for **fatty acid .DELTA.12**

**-desaturases** (oleyl-CoA desaturases) from Arabidopsis

thaliana, Brassica napus, Glycine max, Zea mays, and Ricinus communis was demonstrated. The expression of antisense G. max

**fatty acid .DELTA.12-**

**desaturase** cDNA in soybeans to reduce the expression of the enzyme in developing soybean seeds and use of the cDNA sequences for restriction fragment length polymorphism (RFLP) mapping was also demonstrated.

IC 1CM C12N013-33

IC 1CM C12N013-32; C11E011-1 ; C12Q011-68; A01H005-00

CC 11-1 (Plant Biochemistry)

Section cross-reference(s): 1, 17

ST plant **fatty acid desaturase** cDNA

cloning; breeding lipid compn transgenic plant

IT Plant breeding and selection

cloning of **fatty acid desaturase**

cDNA in relation to)

IT Candi

Soybean

**fatty acid desaturase** expression

vs. antisense cDNA for reduct. of)

IT Protein sequences

of plant microbial **fatty acid**

**desaturases**)

IT Plasmid and Episome

pPh1Fa2R, pZDFa2R, pZK1Fa2R, **fatty acid**

**desaturase** antisense cDNA of Brassica napus on, for expression reduct.)

IT Fats and Glyceridic oils

EL: PRP (Properties)

(transgenic plant cells having altered level of, cloning of

**fatty acid desaturase** in relation to)

IT Plant

(transgenic, unsatd. fatty acid level regulation in, cloning of cDNA for **fatty acid desaturase** in

- relation to)
- IT Deoxyribonucleic acid sequences  
(complementary, for plant microsomal **fatty acid desaturases**)
- IT Deoxyribonucleic acids  
FL: BLOL (Biological study)  
(complementary, antisense, for **fatty acid desaturase**, for reducing **desaturase** gene expression in transgenic plants)
- IT Plasmid and Episome  
pST11, **fatty acid desaturase**  
(antisense cDNA of Glycine max on, for expression redn.)
- IT Genetic polymorphism  
(restriction fragment length, Genetic mapping, of gene for **fatty acid desaturase** of plants, cloning of **fatty acid desaturase** cDNA in relation to)
- IT Fatty acids, biological studies  
FL: PEP (Properties)  
(unsatd., transgenic plant cells having altered level of, cloning of **fatty acid desaturase** in relation to)
- IT 158283-24-0, .delta.-12 **Fatty acid desaturase** (*Arabidopsis thaliana* clone p9113) 158283-26-2, .delta.-12 **Fatty acid desaturase** (*Brassica napus* clone pCF2-165D) 158283-28-4, .delta.-12 **Fatty acid desaturase** (*Glycine max* clone pSF2-16IK) 158283-30-8, .delta.-12 **Fatty acid desaturase** (*Zea mays* clone pFad2#1) 158283-32-0, .delta.-12 **Fatty acid desaturase** (*Ricinus communis* clone pREF-1C) 158283-34-2, .delta.-12 **Fatty acid desaturase** (*Ricinus communis* clone pRF197C-42)  
FL: BLOL (Biological study)  
(amino acid sequence of and cloning of cDNA for, mol. breeding in relation to)
- IT 17-51-31-3, Fatty acid .DELTA.12-hydroxylase  
FL: BLOL (Biological study)  
(gene for, method for cloning of)
- IT 14-51-31-3  
FL: BLOL (Biological study)  
(gene for, of plants, method for cloning of)
- IT 15-11-31-3, cDNA (*Arabidopsis thaliana* clone pAGE2-6 .delta.-12 **fatty acid desaturase** gene)  
FL: BLOL (Biological study); PEP (Properties)  
(nucleotide sequence and cloning of)
- IT 15-11-10-7, cDNA (*Arabidopsis thaliana* clone p92103 .delta.-12 **fatty acid desaturase** cDNA and flanks) 158283-25-1, DNA (*Brassica napus* clone pCF2-165D **fatty acid desaturase** cDNA and flanks) 158283-27-3, cDNA (*Glycine max* clone pSF2-16IK .delta.-12 **fatty acid desaturase** cDNA and flanks) 158283-29-1, DNA (*Zea mays* clone pFad2#1 .delta.-12 **fatty acid desaturase** cDNA and flanks) 158283-31-9, DNA (*Ricinus communis* clone pREF-1C .delta.-12 **fatty acid desaturase** cDNA and flanks) 158283-33-1, DNA (*Ricinus communis* clone pRF197C-42 .delta.-12 **fatty acid desaturase** cDNA and flanks)  
FL: BLOL (Biological study); PEP (Properties)  
(nucleotide sequence and cloning of, mol. breeding in relation

- to)
- IT 141-12-1, Ricinoleic acid  
EL: PRP (Properties)  
(transgenic plant cells having altered level of, cloning of  
**fatty acid desaturase** in relation to)
- L24 ANSWER 13 OF 19 HCAPLUS COPYRIGHT 1997 ACS  
1994:63498L Document No. 121:224-92 Arabidopsis FAD2 gene encodes the  
enzyme that is essential for polyunsaturated lipid synthesis.  
Gutley, John; Lightner, Jonathan; Feldmann, Kenneth; Yadav,  
Narendra; Lark, Ellen; Brown, John (Inst. Biol. Chem., Washington  
State Univ., Pullman, WA, 99164-6340, USA. Plant Cell, 6 1),  
1994- (English) 1994. CODEN: PLOSEW. ISSN: 1040-4651.
- AB The polyunsatd. fatty acids linoleate and alpha.-linolenate are  
important membrane components and are the essential fatty acids of  
human nutrition. The major enzyme responsible for the synthesis of  
these compds. is the plant oleate desaturase of the endoplasmic  
reticulum, and its activity is controlled in Arabidopsis by the  
**fatty acid desatn.** (fad2 locus). A  
fad2 allele was identified in a population of Arabidopsis in which  
**mutations** had been created by T-DNA insertions. Genomic DNA  
fragments the T-DNA was cloned by plasmid rescue and used to isolate  
cDNA and genomic clones of FAD2. A cDNA contg. the entire FAD2  
coding sequence was ~~expressed in fad2 mutant plants and~~  
shown to complement the **mutant** fatty acid phenotype. The  
deduced amino acid sequence from the cDNA showed homol. to other  
plant desaturases, and this confirmed that FAD2 is the structural  
gene for the desaturase. Gel blot analyses of FAD2 mRNA levels  
showed that the gene is expressed throughout the plant and suggest  
that transcript levels are in excess of the amt. needed to account  
for oleate desatn. Sequence anal. identified histidine-rich motifs  
that could contribute to an iron-binding site in the cytoplasmic  
domain of the protein. Such a position would facilitate interaction  
between the desaturase and cytochrome b5, which is the direct source  
of electrons for the desatn. reaction, but would limit interaction  
of the active site with the fatty acyl substrate.
- CC 7-1 Enzymes)
- ST Section cross-reference(s) :  
gene FAD2 oleate desaturase sequence Arabidopsis; cDNA FAD2 oleate  
desaturase sequence Arabidopsis
- IT Arabidopsis thaliana  
(Arabidopsis FAD2 gene for oleate desaturase that is essential  
for polyunsatd. lipid synthesis)
- IT Gene, plant  
EL: BIOL (Biological study)  
(FAD2; Arabidopsis FAD2 gene for oleate desaturase that is  
essential for polyunsatd. lipid synthesis)
- IT Polyunsaturated acid sequences  
(of Arabidopsis FAD2 gene for oleate desaturase)
- IT Enzyme functional sites  
Protein sequences  
(of Arabidopsis FAD2 oleate desaturase)
- IT 141-12-1, Oleate desaturase  
EL: BAC (Biological activity or effector, except adverse); PRP  
(Properties); BIOL (Biological study)  
(Arabidopsis FAD2 gene for oleate desaturase that is essential  
for polyunsatd. lipid synthesis)
- IT 158283-24-0, Oleate desaturase Arabidopsis thaliana clone  
pFAD2 gene FAD2)  
EL: PRP (Properties)  
(amino acid sequence; Arabidopsis FAD2 gene for oleate desaturase  
that is essential for polyunsatd. lipid synthesis)
- IT 15241-16-7  
EL: PRP (Properties)

(nucleotide sequence; Arabidopsis FAD7 gene for oleate desaturase that is essential for polyunsatd. lipid synthesis)

L24 ANSWER 14 OF 19 HCAPLUS COPYRIGHT 1997 ACS

1994:471820 Document No. 121:74829 Identification of conserved domains in the **.DELTA.12** desaturases of cyanobacteria.

Sakamoto, Toshio; Wada, Hajime; Nishide, Ikuo; Ohmori, Masayuki; Murata, Hiroo (Dep. Mol. Biotechnol., Univ. Advanced Studies, Okazaki, 444, Japan). Plant Mol. Biol., 14(4), 643-50 (English) 1991. CODEN: PMBIDE. ISSN: 0167-4411.

AB Cyanobacterial genes for enzymes that **desaturate fatty acids** at the **.DELTA.12**

position, designated desA, were isolated from Synechocystis PCC6714, Synechococcus PCC7002 and Anabaena variabilis by cross-hybridization with a DNA probe derived from the desA gene of Synechocystis PCC6708. The genes of Synechocystis PCC6714, Synechococcus PCC7002 and A. variabilis encode proteins of 149, 147 and 150 amino acid residues, resp. The transformation of Synechococcus PCC7042 with the desA genes from Synechocystis PCC6714, Synechococcus PCC7002 and A. variabilis was assod. with the ability to introduce a second double bond at the **.DELTA.12** position of fatty acids. The amino acid sequence of the products of the desA genes revealed the presence of four conserved domains. Since one of the conserved domains was also found in the amino acid sequences of  $\Delta^6$  desaturases of Brassica napus and mung bean, this domain may play an essential role in the introduction of a double bond into fatty acids bound to membrane lipids.

CC 2-3 (Biochemical Genetics)

Section cross-reference(s): 7, 11

ST desaturase gene desA sequence cyanobacteria; Anabaena Synechococcus Synechocystis desaturase gene sequence

IT Anabaena variabilis

(desaturase gene desA cf, updated nucleotide sequence of)

IT Synechococcus

Synechocystis

(gene desA cf, nucleotide and encoded peptide sequences of)

IT Deoxyribonucleic acid sequences

of desaturase gene desA, of Synechocystis and Synechococcus

IT Protein sequences

of desaturase, of Synechocystis and Synechococcus

IT Gen, microbial

RI: B101 (Biological study)

desA, for desaturase, of Synechocystis and Synechococcus,

nucleotide and encoded peptide sequences of

IT 156532-35-3, Delta 12 desaturase

(Synechocystis PCC714) 156532-36-4, Delta

12 desaturase (Synechococcus PCC7002)

RI: PEP (Properties)

(amino acid sequence of)

IT 156162-28-6 156462-39-6 156471-40-5

RI: B101 (Biological study); PEP (Properties)

(nucleotide sequence of)

L24 ANSWER 14 OF 19 HCAPLUS COPYRIGHT 1997 ACS

1994:184135 Document No. 120:144135 A gene encoding a chloroplast

**omega-3 fatty acid desaturase**

complements alterations in **fatty acid**

**desaturation** and chloroplast copy number of the fad7

mutant of Arabidopsis thaliana. Iba, Hori; Gibson, Sue;

Nishitani, Takumi; Fure, Takashi; Hishinuma, Mitsuo; Arndel,

Valent; Haily, Susanne; Scaevalla, Chris (Fac. Sci., Kyushu Univ.,

Fukuoka, 812, Japan). J. Biol. Chem., 268(3), 24099-105 (English)

1993. CODEN: JBSCHA3. ISSN: 0021-9495.

AB **Mutations** at the fad7 locus of A. thaliana (previously

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called *fadD*) cause decreased **desatn.** of dienoic **fatty acids** in chloroplast lipids in plants grown at elevated temps. This suggested that the *fad7* locus encodes a chloroplast  $\omega$ -3 desaturase that catalyzes the **desatn.** of lipid-linked 18:2 and 16:1 fatty acids. In order to clone the *fad7* gene, it was first genetically mapped relative to the flanking RFLP markers 1047 and 2438A on chromosome 3, and yeast artificial chromosomes covering the locus were identified. A putative desaturase cDNA clone that was isolated by low stringency heterologous probing with a cDNA for an endoplasmic reticulum-localized  $\omega$ -3 desaturase (*fa3*) hybridized to the yeast artificial chromosomes and could not be resolved from the locus by RFLP mapping. Expression of the cDNA in transgenic *fad7* **mutant** plants resulted in restoration of wild-type fatty acid compn. and suppression of a previously obsd. effect of the *fad7* **mutation** in chloroplast n.a. indicating genetic complementation. The structural gene contained seven introns within a coding sequence of 1335 base pairs, which encodes a 446-amino acid polypeptide of 51,172 daltons. The N-terminal region of the *fad7* gene product contained a consensus chloroplast transit peptide. Except for the N-terminal domain, the deduced amino acid sequence of the *fad7* gene product had high homol. to the *fa3* gene product, indicating that *fad7* encodes an  $\omega$ -3 desaturase and that the two genes arose from a common ancestral gene. There was no apparent effect of growth temp. on the steady-state levels of *fad7* mRNA in wild-type plants.

- CC 3-3 (Biochemical Genetics  
Section cross-reference(s) : 7, 11
- ST **fatty acid desaturase** gene; sequence  
Arabidopsis; mapping sequence gene *fad7* Arabidopsis
- IT Arabidopsis thaliana  
(**fatty acid desaturase** gene *fad7*  
of, isolation and sequence and mapping of
- IT Chloroplast  
(**fatty acid desaturase** of,  
Arabidopsis thaliana gene for, isolation and sequence and mapping  
of)
- IT Deoxyribonucleic acid sequences  
of **fatty acid desaturase** gene  
*fad7*, of Arabidopsis thaliana)
- IT Protein sequences  
of **fatty acid desaturase**, of  
Arabidopsis thaliana)
- IT Genetic mapping  
of fatty desaturase gene *fad7*, on Arabidopsis thaliana  
chromosome 3)
- IT Gene, plant  
FL: B10L (Biological study)  
of *fad7*, for **fatty acid desaturase**,  
of Arabidopsis thaliana, isolation and sequence and mapping of)
- IT Chromosome  
(Arabidopsis thaliana), **fatty acid  
desaturase** gene *fad7* mapping)
- IT Peptides, biological studies  
FL: B10L (Biological study)  
(transit, in **fatty acid desaturase**,  
of Arabidopsis thaliana)
- IT 149955-97-5,  $\omega$ -3-Fatty acid  
**desaturase** (Arabidopsis thaliana clone g4)  
FL: PEP (Properties)  
(amino acid sequence of)
- IT 153602-91-4, GenBank S66769  
FL: PEP (Properties)  
(nucleotide sequence of and mapping of)

L24 ANSWER 16 OF 19 HCAPLUS COPYRIGHT 1997 ACS

1994:47043 Document No. 123:47:44 Cloning of higher plant .omega.-3

**fatty acid desaturases.** Yabuta, Narendra

S.; Wierzbicki, Anna; Asperger, Mary; Caster, Cheryl S.; Perez-Grau, Luis; Kinney, Anthony J.; Hitz, William D.; Booth, J. Russell, Jr.; Schweigert, Bruce; et al. (Exp. Stn., E. I. duPont de Nemours and Co., Wilmington, DE, 1988-1992, USA). Plant Physiol., 103(2), 167-76 (English) 1993. CODEN: PLPRAY. ISSN: 0032-1819.

AB *Arabidopsis thaliana* T-DNA transformants were screened for

**mutations** affecting seed fatty acid compn. A **mutant**

line was found with reduced levels of linolenic acid (18:3) due to a T-DNA insertion. Genomic DNA flanking the T-DNA insertion was used to obtain an *Arabidopsis* cDNA that encodes a polypeptide identified as a microsomal .omega.-3 **fatty acid**

**desaturase** by its complementation of the **mutation**.

Anal. of lipid content in transgenic tissues demonstrated that this enzyme is limiting for 18:3 prodn. in *Arabidopsis* seeds and carrot hairy roots. This cDNA was used to isolate a related *Arabidopsis* cDNA, whose mRNA is accumulated to a much higher level in leaf tissue relative to root tissue. This related cDNA encodes a protein that is a homolog of the microsomal desaturase but has an N-terminal extension deduced to be a transit peptide, and its gene maps to a position consistent with that of the *Arabidopsis* *fadD* locus, which controls plastid .omega.-3 levtn. These *Arabidopsis* cDNAs were used as hybridization probes to isolate cDNAs encoding homologous proteins from developing seeds of soybean and rapeseed. The high degree of sequence similarity between these sequences suggests that the .omega.-3 desaturase use a common enzyme mechanism.

CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 7, 11

ST sequence plant **fatty acid desaturase**

gene; *Arabidopsis* **fatty acid desaturase**

gene *fadD*; soybean **fatty acid desaturase**

gene *fadD*; rapeseed **fatty acid**

**desaturase** gene *fadD*

IT Gene, plant

RL: BIOL (Biological study)

*fadD*, for **fatty acid desaturase** of

*Arabidopsis* and soybean and rapeseed, (sequence of)

IT *Arabidopsis thaliana*

*Brassica napus*

Soybean

(**fatty acid desaturases** of

microsomes and chloroplast of, (sequence of genes for)

IT Seed

linolenic acid levels in *Arabidopsis thaliana*, (cloning of

**fatty acid desaturase** gene affecting)

IT Protein sequences

of **fatty acid desaturase**, of

soybean and rapeseed and *Arabidopsis* microsomal and chloroplast)

IT Complementary DNA sequences

complementary, for **fatty acid**

**desaturase**, of soybean and rapeseed and *Arabidopsis*

microsomal and chloroplast)

IT Gene, plant

RL: BIOL (Biological study)

*fadD*, for **fatty acid desaturase** of

*Arabidopsis* and soybean and rapeseed chloroplast, (sequence of)

IT 463-40-1, Linolenic acid

RL: PRP (Properties)

(*Arabidopsis thaliana* seeds with reduced levels of, (cloning of

**fatty acid desaturase** gene causing)

IT 149955-96-4, .omega.-3 **Fatty acid**

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**desaturase** (Arabidopsis thaliana clone CFI gene fad3)  
**149955-97-5, .omega.-3 Fatty acid**  
**desaturase** (Arabidopsis thaliana chloroplast clone CFD gene  
 fadD precursor) **149956-00-3, .omega.-3 Fatty**  
**acid desaturase** (Glycine max clone GMD gene fad3)  
**149956-01-4, .omega.-3 Fatty acid**  
**desaturase** (Glycine max chloroplast clone GMD gene fadD)  
**152208-01-0, .omega.-3 Fatty acid**  
**desaturase** (Brassica napus chloroplast clone BND gene fadD  
 precursor) **152208-02-1, .omega.-3 Fatty**  
**acid desaturase** (Brassica napus clone BN2 gene  
 fad3)

HL: PEP (Properties)  
 (amino acid sequence of)

IT 149955-99-5 149955-99-3 149955-99-9 149955-99-1 151497-59-5  
 151497-60-3

HL: BICL (Biological study); PEP (Properties)  
 (nucleotide sequence of)

L24 ANSWER 17 OF 19 HCAPLUS COPYRIGHT 1997 ACS

1993:418:39 Document No. 119:318:619 Map-based cloning of a gene  
 controlling omega-3 fatty acid

**desaturation** in Arabidopsis. Arendel, Vincent; Lemieux,  
 Bertrand; Hwang, Inwon; Gibson, Sue; Goodman, Howard H.;  
 Somerville, Chris R. (Plant Res. Lab., Michigan State Univ., East  
 Lansing, MI, 48824-1312, USA). Science (Washington, D. C., 1983-),  
 258(5056), 1993-5 (English) 1993. CODEN: SCIEAS. ISSN: 0036-8075.

AB A gene from the flowering plant Arabidopsis thaliana that encodes an  
 .omega.3 desaturase was cloned on the basis of the genetic map  
 position of a **mutation** affecting membrane and storage  
 lipid fatty acid compn. Yeast artificial chromosomes covering the  
 genetic locus were identified and used to probe a Brassica napus  
 seed cDNA library. A B. napus cDNA clone for the desaturase was  
 identified and introduced into roots of both wild-type and  
**mutant** A. thaliana plants by Ti plasmid-mediated  
 transformation. Transgenic tissues of both **mutant** and  
 wild-type plants had significantly increased amts. of the  
**fatty acid** produced by this **desaturase**.

CC 3-3 (Biochemical Genetics)  
 Section cross-reference(s) : 1, 11

ST omega3 desaturase gene mapping Arabidopsis; cDNA omega3 desaturase  
 sequence cloning Brassica

IT Arabidopsis thaliana  
 (gene fad3 for .omega.3 linoleate desaturase of, mapping of)

IT Genetic mapping  
 (of gene fad3 for .omega.3 linoleate desaturase, of Arabidopsis  
 thaliana)

IT Protein sequences  
 (of .omega.3 linoleate desaturase, of Brassica napus)

IT Root  
 (transformation of, of Arabidopsis thaliana, by .omega.3  
 linoleate desaturase cDNA of Brassica napus)

IT Brassica napus  
 (.omega.3 linoleate desaturase cDNA of, sequence and cloning in  
 Arabidopsis thaliana of)

IT Gene, plant  
 HL: BICL (Biological study)  
 (fad3, for .omega.3 linoleate desaturase, of Arabidopsis  
 thaliana, mapping and complementation of)

IT Deoxyribonucleic acid sequence  
 (complementary, for .omega.3 linoleate desaturase, of Brassica  
 napus)

IT Transformation, genetic  
 (transgenesis, of Arabidopsis thaliana roots, by .omega.3

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- linoleate desaturase cDNA of *Brassica napus*)
- IT Chromosome  
*Arabidopsis thaliana* L, gene fad3 for omega.3 linoleate  
 desaturase mapping on)
- IT **148814-49-7**  
 RL: BAC (Biological activity or effector, except adverse); PRP  
 (Properties); BIOL (Biological study);  
 (amino acid sequence of, complete)
- IT 17213-43-6  
 RL: FORM (Formation, nonpreparative)  
 (formation of, by transgenic *Arabidopsis thaliana* expressing  
*Brassica napus* omega.3 linoleate desaturase cDNA)
- IT 148814-49-8, GenBank L01411  
 RL: BIOL (Biological study); PRP (Properties)  
 (nucleotide sequence of)
- L24 ANSWER 13 OF 13 HEADLINES COPYRIGHT 1997 ACS  
 1993:133176 Document No. 112:133176 **Fatty acid  
 desaturase** genes from plants and their use in altering fatty  
 acid composition of plant oils. Browse, John; Grau, Luis Perez;  
Pinney, Anthony J.; Pierce, John W., Jr.; Wierzbicki, Anna M.;  
Yakov, Narendra S. (du Pont de Nemours, E. I., and Co., USA). PCT  
 Int. Appl. WO 9311245 A1 930610, 167 pp. DESIGNATED STATES: W: AU,  
 BR, CA, JP, RU, UA, US; BW: AI, BE, CH, DE, DK, ES, FR, GB, GR, IE,  
 IT, LU, MC, NL, FI, SE. (English). CODEN: PIXXD2. APPLICATION: WO  
 93-0310-4 921313. PRIORITY: US 91-04289 911214.
- AB Elastic and microsomal **delta-15** desaturase cDNAs  
 of *Arabidopsis thaliana*, *Brassica napus*, and *Glycine max* are cloned  
 and sequenced. The effect on 18:2 and 18:3 content of expression of  
 antisense **delta-15** desaturase cDNA in *B. napus*  
 and *G. max* was examd. Use of the cloned cDNA for RFLP anal. and  
 plant breeding was explored.
- IC ICM C110615-5;  
 ICS C110615-33; C112001-11; C112001-63
- CC 3-2 (Biochemical Genetics)  
 Section cross-reference(s): 11, 17
- ST **fatty acid desaturase** cDNA plant  
 sequence; *Arabidopsis* delta15 desaturase cDNA sequence; *Brassica*  
 delta15 desaturase cDNA sequence; *Glycine* delta15 desaturase cDNA  
 sequence; oil glyceridic plant unsatd fatty acid; RFLP plant  
 breeding desaturase cDNA
- IT Plant breeding and selection  
 RFLP anal. in plant **.DELTA.-15**  
**fatty acid/glycerolipid desaturase**  
 (cDNA for)
- IT Gene, plant  
 RL: BIOL (Biological study)  
 (for **.DELTA.-15 fatty acid**  
 glycerolipid **desaturase** of *Arabidopsis thaliana* and  
*Brassica napus* and *Glycine max*)
- IT Protein sequences  
 (of **.DELTA.-15 fatty acid**  
 glycerolipid **desaturase** of *Arabidopsis thaliana* and  
*Brassica napus* and *Glycine max*)
- IT Plant  
 (oil-producing, alteration of linolenic acid content of  
 transgenic, cloning of plant **.DELTA.-15**  
 desaturase cDNA in relation to)
- IT *Arabidopsis thaliana*  
*Brassica napus*  
*Cocoa* (*Theobroma cacao*)  
 Corn  
 Cotton  
 Peanut

Safflower  
Soybean  
Sunflower

(plant **.DELTA.-15 fatty**

**acid/glycerolipid desaturase** cDNA expression

in, for alteration of linolenic acid content of oil)

IT Fat and Glyceridic oils

HL: BIOL (Biological study)

with altered linolenic acid content, transgenic plants

producing, cloning of plant **.DELTA.-15**

**desaturase** cDNA in relation to

IT Deoxyribonucleic acid sequences

complementary, for **.DELTA.-15 fatty**

**acid/glycerolipid desaturase** of *Arachidopsis*

*thaliana* and *Brassica napus* and *Glycine max*)

IT Genetic polymorphism

restriction fragment length, of plant genomes, plant

**.DELTA.-15 fatty acid**

**glycerolipid desaturase** cDNA for anal. of:

IT 149955-96-4, **.DELTA.-15 Desaturase**

(*Arachidopsis thaliana* clone pCF3; 149955-97-5,

**.DELTA.-15 Fatty acid**

**desaturase** (*Arachidopsis thaliana* clone pACE2-1 plastid)

149955-98-6, **.DELTA.-15 Glycerolipid**

**desaturase** (*Brassica napus* clone pBNSF3-2 microsomal)

149955-99-7, **.DELTA.-15 Glycerolipid**

**desaturase** (*Brassica napus* clone pBNSF4-2 plastid)

149956-00-3, **.DELTA.-15 Desaturase**

(*Glycine max* clone pXF1 microsomal) 149956-01-4,

**.DELTA.-15 desaturase** (*Glycine max* clone

pSFD-118bwp plastid) 149956-02-5, **.DELTA.-**

**15 desaturase** fragment (*Zea mays* clone pCF20,

149956-03-6, **.DELTA.-15 Desaturase**

fragments (*Arachidopsis thaliana* clone pFack-2 plastid)

HL: PEP (Properties)

amino acid sequence of

IT 149955-8-3, DNA (*Arabidopsis thaliana* clone pCF3 **.DELTA.-**

**15 desaturase** cDNA and flanks) 149955-91-3, DNA

(*Arachidopsis thaliana* clone pACE2-2 plastid **fatty**

**acid .DELTA.-15 desaturase**

cDNA and flanks) 149955-91-3, DNA (*Brassica napus* clone pBNSF3-2

microsomal **.DELTA.-15 glycerolipid desaturase**

cDNA and flanks) 149955-92-1, DNA (*Glycine max* clone pXF1

microsomal **.DELTA.-15 desaturase** cDNA and

flanks) 149955-93-1, DNA (*Glycine max* clone pSFD-118bwp plastid

**.DELTA.-15 desaturase** cDNA and flanks)

149955-94-2, DNA (*Zea mays* clone pCF20 **.DELTA.-15**

**desaturase** cDNA) 149955-95-3, DNA (*Arachidopsis thaliana* clone

pFack-2 plastid **.DELTA.-15 desaturase** cDNA)

HL: BIOL (Biological study); PEP (Properties)

nucleotide sequence of, use in RFLP anal. and in transgenic

plants for alteration of fatty acid content of oils of)

IT 46-46-1, Linolenic acid

HL: PEP (Properties)

transgenic plants producing oil with altered levels of, cloning

of plant **.DELTA.-15 desaturase** cDNA in

relation to)

L24 ANSWER 13 OF 19 HEADPLUS COPYRIGHT 1997 ACS

1991:18174 Document No. 114:1-574 The OLE1 gene of *Saccharomyces*

*cerevisiae* encodes the **.DELTA.9 fatty acid**

**desaturase** and can be functionally replaced by the rat

stearoyl-CoA desaturase gene. Stuckey, Joseph E.; McDonough,

Virginia M.; Martin, Charles E. (Nelson Biol. Lab., Rutgers, State

KATHLEEN FULLER BT/LIBRARY 308-4290

Univ., Piscataway, NJ, 08855-1059, USA). J. Biol. Chem., 265(33), 20144-9 (English) 1990. CODEN: JBCHA3. ISSN: 0021-9258.

AB Strains of *S. cerevisiae* bearing the *ole1* **mutation** are defective in unsatd. fatty acid (UFA) synthesis and require UFAs for growth. A previously isolated yeast genomic fragment complementing the *ole1* **mutation** was sequenced and found to encode the **DELTA-9 fatty acid desaturase** enzyme by comparison of primary amino acid sequence to the rat liver stearyl-CoA desaturase. The *OLE1* structural gene encodes a protein of 513 amino acids (2.1 kDa) having an approx. mol. mass of 55.4 kDa. A 357-amino acid internal region of the yeast open reading frame aligns with and shows 88% identity and 63% similarity to the rat liver stearyl-CoA desaturase protein. This comparison disclosed 3 short regions of high conservative amino acid identity (70%) including one 11 of 12 perfect residue match. The predicted yeast enzyme contains 4 potential membrane-spanning regions and several shorter hydrophobic regions that align exactly with similar sequences in the rat liver protein. An *ole1* gene-disrupted yeast strain was transformed with a yeast-rat chimeric gene consisting of the promoter region and N-terminal 27 codons of *OLE1* fused to the rat desaturase coding sequence. Fusion gene transformants displayed near equiv. growth rates and modest lipid compn. changes relative to wild-type yeast control implying a significant conservation of **DELTA-9** desaturase tertiary structure and efficient interaction between the rat desaturase and yeast cytochrome b5.

CC 1-3 (Biochemical Genetics)

Section cross-reference(s): 7

ST **fatty acid desaturase** gene sequence

*Saccharomyces*; gene *OLE1* sequence *Saccharomyces*

IT *Saccharomyces cerevisiae*

(**fatty acid desaturase** gene *OLE1*)

cf, nucleotide and encoded peptide sequences of)

IT Endoplasmic reticulum

(**fatty acid desaturase** insertion)

into cell membrane of, of *Saccharomyces cerevisiae*)

IT Protein sequences

(of **fatty acid desaturase**, of

*Saccharomyces cerevisiae*, complete

IT Fatty acids, biological studies

Lipids, biological studies

EL: BIOL (Biological study)

(of transformed *Saccharomyces cerevisiae* contg. **fatty**

**acid desaturase** gene

IT Complementation, genetic

stearyl CoA desaturase gene in, of yeast cells contg.

**mutant fatty acid desaturase**

genes)

IT Fat

stearyl CoA desaturase gene of, in complementation of

*Saccharomyces cerevisiae* contg. **mutant fatty**

**acid desaturase** gene)

IT Long-chain fatty acid sequences

stearyl CoA desaturase-specifying, of *Saccharomyces cerevisiae*,

(complete)

IT Fatty acids, biological studies

EL: BIOL (Biological study)

unsatd., of transformed *Saccharomyces cerevisiae* contg.

**fatty acid desaturase** gene)

IT Gene and genetic element, microbial

EL: BIOL (Biological study)

*OLE1*, for **fatty acid desaturase**,

of *Saccharomyces cerevisiae*, nucleotide and encoded peptide

sequences of)

IT 131198-85-1  
 FL: PRP (Properties)  
 (amino acid sequence of)  
 IT 9014-34-0, DELTA-9 Fatty acid  
 desaturase  
 FL: PRP (Properties)  
 gene for, of Saccharomyces cerevisiae, structure and  
 complementation anal. of)  
 IT 131198-85-9, Deoxyribonucleic acid (Saccharomyces cerevisiae gene  
 CLE1)  
 FL: BIOL (Biological study); PRP (Properties)  
 (nucleotide sequence of)  
 IT 57-11-3, Fatty acid 16:0, biological studies 57-11-4, Octadecanoic  
 acid, biological studies 112-50-1, 9-Octadecenoic acid (Z)-,  
 biological studies 573-49-9 544-63-1, Tetradecanoic acid,  
 biological studies  
 FL: BIOL (Biological study)  
 (of transformed Saccharomyces cerevisiae contg. fatty  
 acid desaturase gene)

=> sel hit rn 1-19

E1 THROUGH E36 ASSIGNED

=> file reg

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 SEL HIT RN 1-19

FILE 'REGISTRY' ENTERED AT 11:41:12 ON 18 DEC 1997

L25 16 S E1-E36

=> s 15 and 125

L26 36 L5 AND L25

=> d 126 sqide can

L26 ANSWER 1 OF 36 REGISTRY COPYRIGHT 1997 ACS  
 RN 197594-15-3 REGISTRY

KATHLEEN FULLER BT/LIBRARY 308-4290

• CN Desaturase, oleoyl coenzyme A (Petroelinum crispum clone ELI12)  
(CI) CA INDEX NAME

## OTHER NAMES:

CU GenBank U66374-derived protein GI 2101792

PS PROTEIN SEQUENCE

SQL 383

```

SEQ      1 MDAAGGHSISIP PIVKTAASA IKRAPHEKEP ETIGILKKAI PAHCFQKSLV
      51 TSPRYLIQDL PMAYALFTVA TNYIDQILET PENYVAAWAA IAVQGEVLTG
     101 AWVVEHCIEH DAFQNYNWIN DADGLVTESS LLYPYFSWHI SHRAHHANTQ
      ==  ==
     151 SIENDEFTVP RPHSNIRNYY ELINNEPGGV LKWLITLIG FPLYIMFNVS
     201 GMYEHWTEH YDREPLYSD EERKEIIVSD IAILAVIYDL YQLVLAAGEA
      ==  ==
     251 WYFQVYQGLL LVAIGWFYLY TLNHNHNSL FYNDSTEWIW LEGALCTVDR
     301 DQGLNKEH DADARVCHH LPSHHPHYRG DECTFAMHFI LGEYTPQDGT
      ==  ==
     351 PLKAMYREH PHTIYVENDE GETEGUYWEH NKF

```

HITS AT: 106-110, 141-146, 113-114, 116-120

MF Unspecified

CI MAN

SA CA

LC STM Files: CA, CAPLUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 1.7:11084

and 1.7 sqds. can. 2-3.

L26 ANSWER 1 OF 36 REGISTRY COPYRIGHT 1991 ACS

EN 197594-14-2 REGISTRY

CN Desaturase, fatty acid omega.3- Petroelinum crispum clone 15-1)  
(CI) CA INDEX NAME

## OTHER NAMES:

CU GenBank U66374-derived protein GI 1789066

PS PROTEIN SEQUENCE

SQL 438

```

SEQ      1 MAAWVIFPGG IRIIFRIYAR IRGAGJCFNS EHVVENLEFL DENVKICHTG
      51 CEMWGLIYVSU IMNVFSVNEF EEPFECINEE ENEFIPGLAP PEKESINFAA
     101 IPEHOWYDFD VEMISYVIED VLIYFELAVA ASFVNKNKAW PLYWIAQGTG
     151 PWALPVLGHD CGHGSFSDA FLNIVGHIL EESILVFYEG WRISRETRHQ
      ==  ==
     201 DEGHVENES WHFIREKLEN TLGLTKKFR ETEFPMLAY PFYLWGRSPG
      ==  ==
     251 KGGSHYTFSS ILEVFNKKL VITVTCWTA MAALLVGLDF VMGPVNLML
     301 VGIPYWIYVH WLPVITYLHH EGEDELEWY EGHEWSYLFQ GLTTLDRDYG
      ==  ==
     351 WINNIHHDIG EKHHLHPQ IPEYRLIAT EAQIVFGFY YEPHNSGPV
      ==  ==
     401 PFHLLALWK FEPDEFUSD TGIWVYIQAQ PETANTQN

```

HITS AT: 119-161, 19-112, 319-323, 362-366

MF Unspecified

CI MAN

SA CA

LC STM Files: CA, CAPLUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 1.7:31084

L26 ANSWER 3 OF 36 REGISTRY COPYRIGHT 1991 ACS

KATHLEEN FULLER BT LIBRARY 308-4290

EN 196217-80-8 REGISTRY  
 CN 384-721-Desaturase, oleate (Corylus avellana clone I) (9CI) (CA  
 INDEX NAME)  
 ES PROTEIN SEQUENCE  
 SQL 338

SEQ 1 QEQLLSSPSY VVYDLSLAPL FTYIATSYFH LIPHPLELYA WSIYWALQGC  
 = == =  
 51 LTGFWAVIAH EDSHHAESDY QWYDMVGLT DEVALNPYF SWKISHCRHH  
 == == ==  
 101 SUTGSLDDEE VVYFPPSSH PWYFPPSH PGRVLTGLIT LTGFWFLYLA  
 131 LKPSRPYD PAVHYDPYGP LYNIEKQDI EVDAGVFAT TYVLYAAMS  
 161 PGLAWLTYF GMLLLVNGE LVLITVQRT HPALPHYDGS EWDWLEGALA  
 191 TAQRDYKMLN KVFYVLDTH VAKHLFSTIP HYRAMEATRA IKSILCKYYQ  
 == == ==  
 201 FDTFPTVYK WKEAFGLYV EVDGAPNES VEWYQSEL

HITS AT: 31-64, 65-69, 90-100, 103-204

MF Unspecified

CI MAN

SE CA

SC STM Files: CA, CAPLUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 117:15-443

1.6 ANSWER 4 OF 10 REGISTRY COPYRIGHT 1997 ACS

EN 196217-78-4 REGISTRY

CN Desaturase, oleate (Corylus avellana clone N2 gene PAD2-N) (9CI)  
 (CA INDEX NAME)

ES PROTEIN SEQUENCE

SQL 382

SEQ 1 DGAGSRMFAT HNEPQSTPI QWANTHDEF TLGQLKFAVP PNCQPSSEL  
 51 SFQYVYIS LASFYTYIAT YFHLPHSL CYLAWNTYWA LGGLLTGVW  
 (1000000000)  
 101 VIANECGHH AFSDYQWLDD TVGLIFHSFL LVPYFQWKEYS HRRHHSNTGS  
 == == ==  
 151 LKPSRPYD PAVHYDPYGP LYNIEKQDI EVDAGVFAT TYVLYAAMS  
 181 PYDFPCHYD PPGYYSNPF EQLFYSIAG VFATYVLLY AMHKGLAWL  
 211 VVYFCHLIT VDFVAVITV LGTHPAIHF VVSEWVLR GALATADEY  
 241 GMLLLVNGE LVLITVQRT HPALPHYDGS EWDWLEGALA  
 (1000000000)  
 251 VVYFCHLIT VDFVAVITV LGTHPAIHF VVSEWVLR GALATADEY

HITS AT: 33-66, 104-106, 140-144, 214-215

MF Unspecified

CI MAN

SE CA

SC STM Files: CA, CAPLUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 117:15-443

1.6 ANSWER 5 OF 10 REGISTRY COPYRIGHT 1997 ACS

EN 192889-81-9 REGISTRY

CN Desaturase, oleoyl-cochlar (Brassica napus clone Q50 isoenzyme F)  
 (9CI) (CA INDEX NAME)

ES PROTEIN SEQUENCE

SQL 384

SEQ 1 DGAGSRMFAT HNEPQSTPI QWANTHDEF TLGQLKFAVP PNCQPSSEL  
 51 SFQYVYIS LASFYTYIAT YFHLPHSL CYLAWNTYWA LGGLLTGVW  
 101 VIANECGHH AFSDYQWLDD TVGLIFHSFL LVPYFQWKEYS HRRHHSNTGS  
 KATHLEEN FULLER BT LIBRARY 300-4290

```
=====
151 LERDEVEFVPH KKSDFWYGH YRNNPLGRIV MLTVQFTLGW PLYLAFNVSG
201 RPYDGGFACH FPHNAPIYND RERLQIYISD AGILAVCYSL YRYAAVQGVA
251 SHTCFYGYPL LITGHFLVLI TYLQHTHPSL PHYDSSEWVW LEGALATVDE
301 IYGLNENYFH NITLTHVAHH LESTMPHYHA MEATFAIKFI LGEYYQIHGT
=====
```

351 IYKAMWSEA HFCIYVERDE QGEMFGVFWY INEL

HITS AT: 130-135, 141-145, 316-321

MF Unspecified

CI MAN

SR CA

LC STM Files: CA, CAPLUS

1 REFERENCED IN FILE CA (1967 TO DATE)

1 REFERENCED IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 137:135001

126 ANSWER 6 OF 10 REGISTRY COPYRIGHT 1997 ACS

EN 192889-79-5 REGISTRY

CN Deaturase, phenylalanine (Brassica napus strain Westar asoenzyme F) (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE

SQL 384

```
SEQ 1 MGAAGGMAVS HFFHSEBTDI IKNHCHTEI FTUGELFKAI PPHCFEESIF
51 RPSFYLIKDI IACDFYYHA TTYHLLERH LSYFAWELW AQQGCYLTGV
101 WYLAHNDYHH APTTYQWLDI TYGLIHSFI LVPYFSWYYS HSHHNTTGS
=====
151 LERDEVEFVPH KKSDFWYGH YRNNPLGRIV MLTVQFTLGW PLYLAFNVSG
101 RPYDGGFACH FPHNAPIYND RERLQIYISD AGILAVCYSL YRYAAVQGVA
151 SHTCFYGYPL LITGHFLVLI TYLQHTHPSL PHYDSSEWVW LEGALATVDE
101 IYGLNENYFH NITLTHVAHH LESTMPHYHA MEATFAIKFI LGEYYQIHGT
=====
```

351 IYKAMWSEA HFCIYVERDE QGEMFGVFWY INEL

HITS AT: 130-135, 141-145, 316-321

MF Unspecified

CI MAN

SR CA

LC STM Files: CA, CAPLUS

1 REFERENCED IN FILE CA (1967 TO DATE)

1 REFERENCED IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 137:135004

126 ANSWER 7 OF 10 REGISTRY COPYRIGHT 1997 ACS

EN 192889-77-3 REGISTRY

CN Deaturase, phenylalanine (Brassica napus clone IMC129 asoenzyme D) (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE

SQL 384

NTE

type	location	description
uncommon	A13-69	-

```
SEQ 1 MGAAGGMAVS HFFHSEBTDI IKNHCHTEI FTUGELFKAI PPHCFEESIF
51 RPSFYLIKDI IACDFYYHA TTYHLLERH LSYFAWELW AQQGCYLTGV
101 WYLAHNDYHH APTTYQWLDI TYGLIHSFI LVPYFSWYYS HSHHNTTGS
=====
151 LERDEVEFVPH KKSDFWYGH YRNNPLGRIV MLTVQFTLGW PLYLAFNVSG
201 RPYDGGFACH FPHNAPIYND RERLQIYISD AGILAVCYSL YRYAAVQGVA
251 SHTCFYGYPL LITGHFLVLI TYLQHTHPSL PHYDSSEWVW LEGALATVDE
```

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301 DYGILNKVFH NITDTHVAHH PEETMPHYHA NEATKAIKPI LGEYYQFDST

=====

51 PUVKAMWEEA KECIVVEPDR QGEEKGVFWY NNEL

HITS AT: 1-3-103, 141-143, 316-319

MF Unspecified

CI MAN

CE CA

CC STM Files: CA, CAPLUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 11:137034

1.6 ANSWER 1 OF 36 REGISTRY COPYRIGHT 1997 ACS

EN 192889-75-1 REGISTRY

CH Desaturase, oleoyl-coA: (Brassica napus strain Westar isoenzyme  
D) (9CI) (CA INDEX NAME)

FI PROTEIN SEQUENCE

SQL 384

NTE

type	location	description
uncommon	Asa-63	-

SEQ 1 MGAGGAMWVS DFTKKEBIDT LKATPCTETP FTUGELKKAI PRHCTEPSIP  
51 KPSYLIWDI LKACPYWYA TITPFLIPHP LSYFAWPIW ACQGCVLTSV  
101 WUAREGCHH ARSDGQWDE TIGLIERSEL LVEYFHWYS HPSHHNTGS  
=====

151 LREDEVYFK KESDHWYOK YLNEFLGRTV MLTWQFELGW PLYLAENVSG  
301 RPYCGGFCH PHHMAIYND EELIQIVIS AGILAVCYGL FRYAACQGVA  
451 SINGTCGPH LNVGHVAM TYNQTHPSL PHYDSEEWLW FEGALAIQDS  
301 DYGILNKVFH NITDTHVAHH PEETMPHYHA NEATKAIKPI LGEYYQFDST  
=====

51 PUVKAMWEEA KECIVVEPDR QGEEKGVFWY NNEL

HITS AT: 1-3-103, 141-143, 316-319

MF Unspecified

CI MAN

CE CA

CC STM Files: CA, CAPLUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 11:137034

1.6 ANSWER 1 OF 36 REGISTRY COPYRIGHT 1997 ACS

EN 186208-06-0 REGISTRY

CH Desaturase, DELTA-4-Fatty acid (Pichia angusta) (9CI) (CA INDEX  
NAME)

FI PROTEIN SEQUENCE

SQL 451

SEQ 1 MGRSHNTMT ARKLEPSSIA NMLAPDELEK NPYLQFHS EQPWTWINWH  
51 KHNWVNFIL VNAVFAQIL STFWVPLKLE TPTAVILNC FEGISITAGY  
101 HARWANRAYD QELPKIFFA LQVSAVEGS IHWQHQHV HERYIDTPRO  
=====

151 PYDAKGFQWY SHMGMLNLP NRYKARADI SDLLQWVVR VQRRHYLLM  
301 VMASTFPAY LCHYLNDFW GGFYACLE AVTIQATEC VNELAHWIGE  
231 QPFDGERTPE DEVLATATF GQYHNHREH FNDYRNALK WYQYDPTKV  
=====

301 IYLLSEYHA YULKEFSQNA IDQILQQQQ KNDDEMRAL NWGPQLSELP  
351 VWDKSTFFER AKSDQGLVII SLVHDVANT LTERPGQAL LKTSFGIDAT  
401 MAFNGGYAH SNAAHNLIAT MKVAVIRDCG ANQDTFAQL RYLAKENEF

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451 E

HITS AT: 138-142, 275-279

MF Unspecified

CI HAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 126:113911

126 ANSWER 11 OF 36 REGISTRY COPYRIGHT 1997 ACS

RN 180583-92-0 REGISTRY

CN Desaturase, linoleate (Boraginaceae officinalis) (PCI) (CA INDEX NAME)

PS PROTEIN SEQUENCE

SQL 448

```

SEQ      1 MAAQIKKQIT SDLENHETKE EDWIRIQKE AYVSDWVMD HPGGSFPLKS
      51 LAGQNTDWF VAFHASTWK NIDHFTGYV LKDYVSSENS KDYRKLVFHE
     101 SPMGINTKKS RIMEATLOFI AMLEFMSVYG VLECEGVLEH LEFGQINGFL
     151 WIQSWIGHD AGHVMVVDG ELNKEHGIKA ANCLGGISIG WKKWHHNAHE
      201 IACNMLENDE LQQTPEIIV SKEFFGLTS HYTEKLTED SLSEPFVSYQ
     251 HWTFYPIHMA AALUMYVQSL IMILTERNVS YRAQELLGEL VFSIWYPLIV
     301 SCLPWRGRI KVTIASLVI ENQOVQPSIH HFSSEYVVK PKGNWFERQ
     351 TDGMDIIE EPMHWPHGGG QFOIEHLEP KIFECLEKI SPYVIELOKE
     401 HNLPHYALF SEACEMERT LKITALQAD ITFPLPMIV WEALHTG

```

HITS AT: 158-163, 196-199

MF Unspecified

CI HAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 170:289090

REFERENCE 2: 170:161300

126 ANSWER 11 OF 36 REGISTRY COPYRIGHT 1997 ACS

RN 175960-67-5 REGISTRY

CN Oxidase, lipoate (Arabidopsis thaliana clone pFL6102) (PCI) (CA INDEX NAME)

PS PROTEIN SEQUENCE

SQL 281

```

SEQ      1 MAADNAYLDQ FVDETSEYNE IYICHLLEAI LWFPIPEFLQ TWLRNYLAGT
      51 LLYLISGFHW CFYTYFERIN VYLSKLAIFT IKAMFLQNEV AMKAMPWYTL
     101 LETVSEHIE EGWYCEASI GRFOWILYIV YIAIYLFVE FGIYWHREEL
      151 HDIKPLKTEL HATHHEYNQ NDLSEACIA FHEVGLLQA VPEVIALFIV
     201 HIFETTHGL LEMALWAAN IEDALGNIV PMGAGYH.I HHTTYKENYG
     251 HYTIWHEWF GLRIQLLES DINKDSEKFA E

```

HITS AT: 147-151, 161-163, 203-207, 222-226, 231-232, 247-251

MF Unspecified

CI HAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:30005

LM6 ANSWER 12 OF 26 REGISTRY COPYRIGHT 1997 ACS  
 EN 168613-13-6 REGISTRY  
 CH Desaturase, fatty acyl coenzyme A (Anacystis nidulans strain P2-SPc reduced) (9CI) (CA INDEX NAME)  
 OTHER NAMES:  
 CH Desaturase, acyl coenzyme A (Synecococcus strain PCC 6801)  
 EC PROTEIN SEQUENCE  
 SQL 278

SEQ 1 MTHAIRPRLA EEWPTALEMV AIHIGALLAF LPANFNWPAV GVMVALTYIT  
 51 GDFGHTLQWH ELISHASPEV EKWLEYVLVF CGTLAIQHGP IENIGLRRHH  
 =====  
 101 HHSIQEQTH HEDNNGELWS EPLMNIYEIF ARCEVDEFTF DIASDEMYEF  
 =====  
 151 EKKYPTCTQV LIAVLLYAWL EAWVCGWSEF VVWGIFARLV VVTHVTLVN  
 201 SATHPQETLS HEGDQSTND WWVALLAFGE GWNNNGHAYQ YSARHCLQWW  
 =====  
 251 EFDLTWIND GIKKALARK IFVASPNN

HITS AT: 97-100, 102-107  
 MF Unspecified  
 CI MAH  
 SE CA  
 DC STM Files: CA, CAPLUS  
 1 REFERENCES IN FILE CA (1967 TO DATE)  
 1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:30006

LM6 ANSWER 13 OF 26 REGISTRY COPYRIGHT 1997 ACS  
 EN 163961-98-6 REGISTRY  
 CH Desaturase, fatty acid omega.6- Arabidopsis thaliana gene fad6) (9CI) (CA INDEX NAME)  
 EC PROTEIN SEQUENCE  
 SQL 418

SEQ 1 MASEIALQNF AFITGTCQLF EYFELAASSA EYFPGVYAVK PIDLMIKRT  
 51 HNEFEQYAVV KFFIGCIKAV AATVAPPSAD SAFDFQLAE SYGERQIGED  
 101 LPEYVTHKTI MCLPSEVES IDLKALESV LNVICYTIG LEHIAKSPWY  
 151 LILPLAWWIG TAITGEFTIG HICAKSESEK NELVEDIVCT LAFLPIVYFY  
 =====  
 201 EHWFEHLEH NANTMLYHD TAWQHPPEE FENSPVMRFA IIPSYQIRP  
 =====  
 251 WSHIAWQWV HENLSEFFAS EVNEVKISLA QVFATIAVGV PLIVYVNGIL  
 301 GWNFEWIGW LGYHFMSTF TMTHETAPHI PYPALAEWNA AQAQLNGIVH  
 =====  
 351 QDYFQWIEL CHINVEIPE HISPRIPSYN LEAARFSIQE NWGKYTNLAT  
 =====  
 401 WNWREIMFTM CDHUYDF

HITS AT: 171-173, 175-177, 221-229, 367-371  
 MF Unspecified  
 CI NEM  
 SE CA  
 DC STM Files: CA, CAPLUS  
 1 REFERENCES IN FILE CA (1967 TO DATE)  
 1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:38103

LM6 ANSWER 14 OF 26 REGISTRY COPYRIGHT 1997 ACS  
 EN 161027-24-3 REGISTRY  
 CH Desaturase, fatty acid DELTA.15- (Synecococcus sp. PCC 6803 clone pbluescript/6.0-kbp gene desB) (9CI) (CA INDEX NAME)  
 KATHLEEN FULLER BT/LIBRARY 503-4290

## OTHER NAMES:

CU Omega-3 Desaturase (Synchocystis sp. PCC 6803 clone  
pBlueScript/5.6-kbp gene desP)  
CU GenBank D00012-derived protein GI 1601333  
CU Protein (Synchocystis strain PCC 6803 clone  
csl0687) in pSL1001 (csl025, csl0391 open reading frame sll1441  
reduced)  
EU PROTEIN SEQUENCE  
SQL 359

SEQ 1 MELKISQPT KIPYKRIEEL PFTIQELENA IPADPEPSV VRSLGYFFLD  
11 KGLIAGPTAL AAYKDWFTY EIEWLIQGL FWCLEFVGHG CGHSSPSKSK  
=====

101 TLNWKIGHS HTPIKETHG WRISHRTHA NTGNIDIDES WYPVSEQKYN  
=====

101 QHAWYKELR EYLPICAYPI YLFEASNNQ GSHFMGSSPL EEPDEKAAVL  
101 SSTFALAAFY ELGGLTWQF GWLEFLKFTY APYLVEFWWL DLVTELHETE  
101 LKIPWYHSD WYFIKCALST IDRYGFIH IHDIGIHVA HRIFSNMFY  
=====

101 KLRGAEATK ILGSEYTRYS DEPIWQAPPK SYNACHEFVN QGSEVYYQSP  
101 LGGGTQKRP

HITS AT: 13-14, 15-18, 28-29

MF Unspecified

CI NAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 13:70-81

REFERENCE 1: 12:11,984

136 ANSWER IS OF 3 REGISTERED COPYRIGHT 1997 ACS

EU 158651-91-3 REGISTRY

CU Desaturase, fatty acid omega-3- (Arachidopsis thaliana clone DES1  
plastic-associated isoenzyme) (BCI: CA INDEX NAME)

## OTHER NAMES:

CU Desaturase, fatty acid omega-3- (Arachidopsis thaliana gene fad8)  
EU PROTEIN SEQUENCE  
SQL 435

SEQ 1 MASNINTEG EEPLEFVEYK HTTSEASNF PTFYFNEPLK EPEELNSEN  
11 QFYPTFMA LKWTFLITL QSPSEELTFP FPGALFFN LADIRAAIPK  
101 EOWYFHWK DEYTFIMAI YFGLAAYAY FNIWLNWPLY WFAQGTMEWA  
101 LKVIQKICGH QFPCHEELN YVAGELLRCS ILNPHYGWEL SHFTHHQNHG  
=====

101 HYENDESWHP LPEAIYHLE KITQMERETI PEINLAYPFY LWNESPGFQG  
101 LHYHEDQDF LPEKHTVLT STACWTAMA LKCNFVMG FIQELKLYGI  
101 PEWIPATWLD EWTILHHGR HDKLEWYRCF EWNYLGGLT TLDSDYWIN  
=====

101 NHHHGGTHV LHHHQQPQK YHIVEATEAA KPVICHYYRE PKNSSPLPLH  
=====

101 LGGSNLYNE LQHEKDTGD VVYYEADPH NGORT

HITS AT: 16-18, 19-19, 316-320, 359-363

MF Unspecified

CI NAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 12:26,91

REFERENCE 2: 101:207100

REFERENCE 3: 101:249101

L26 ANSWER 16 OF 36 REGISTERED COPYRIGHT 1997 ACS

EN 158283-34-2 REGISTERED

CN Desaturase, oleoyl coenzyme A (castor-oil plant clone pRF197C-42 reduced) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN .delta.-11 Fatty acid desaturase (Ricinus communis clone pRF197C-42)

ES PROTEIN SEQUENCE

SQL 387

```

SEQ      1 MGGGSRMSTV ILSNSENKQ CSNHLERAPH TTPYTLGNL KFAIPPHCFE
      51 KSPYSSFSNF AYNPCISPLS YSIATNEFFY ISPLSYVAW LUYWLFQGC I
     101 MGLWVICHF CCHHAPSEYQ LADDIVGLIV HSALLVPYFS WKYSHERHHS
      131 HIGLEHEDV FVPSPTNHS WYKYLNNPP GRULTLAATL LLGWPLYLAF
     101 NVGSEYDHF AWHYDIYGP I PSNEERLQIY IADLCIFAT FVLYQATMAK
     151 GLAKVMEIYS VPLNIVRPL VMTYLQSTH PAIPYESSSE WDWLRGAMVT
     201 VDEGCGELNH VERNIALDTRV AHHLEATVPH YHAMEATRAI PTMGSEYRY
      231 DGTFFYALW SHASECLAVE IDECAPTQGV FWYRNKY
  
```

HITS AT: 108-110, 108-109, 108-107

NE Unpublished

CI MAM

SE CA

IC STM Files: CA, CAPUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPUS (1967 TO DATE)

REFERENCE 4: 101:200000

L 6 ANSWER 17 OF 36 REGISTERED COPYRIGHT 1997 ACS

EN 158283-32-0 REGISTERED

CN Desaturase, oleoyl coenzyme A (castor-oil plant clone pFad1 2.4-amin acid fragment reduced) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN .delta.-11 Fatty acid desaturase (Ricinus communis clone pF2-1C)

ES PROTEIN SEQUENCE

SQL 224

```

SEQ      1 WYKARDGHH ANNYQLDDO VVGHILHSL LUYVESWHS HERHHNTGS
      51 LRESEVPHK FKNVFWYSK YLNNPPGRIM TIAVLELGW ILYLAENVSG
     101 KPYGFWYHT LHTGPIYHDE ERIRIFISDA GVLAVTEGLY QLAIAFGIAW
     151 VVCTYCHLL VCKFLVHIT FLQSTHPALP HYDSSEKDWL FGALATVDED
     201 YGILNETHY ITDTQVAHHL PTH
  
```

HITS AT: 108-110, 108-107

NE Unpublished

CI MAM

SE CA

IC STM Files: CA, CAPUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPUS (1967 TO DATE)

REFERENCE 1: 101:200000

L26 ANSWER 18 OF 36 REGISTERED COPYRIGHT 1997 ACS

EN 158283-30-8 REGISTERED

CN Desaturase, oleoyl coenzyme A (corn clone pFad21 reduced) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN .delta.-12 fatty acid desaturase (Zea mays clone pFad2#1)

KATHLEEN FULLER BT/LIBRARY 308-4290

ES PROTEIN SEQUENCE  
SQL 387

```
SEQ      1 MGAGSEMTPEK ERENQEQALAP ATGGAAMQES PVEKPFPTLG QIKKAIPPHC
      51 PERSNIPTET YVHOLNIAA ALLYFALAH I PAIPSPERYA AWPLYWIAQG
     101 CYSTGVWVIA HEDSHHAFSI YSLIDVAVOL VLRFSLINPY FSWHYCHREH
      151 HCHTGSIERD ENFVPEPYEA LPWITIIVYN NPAGEVTHIV VQLTDWPLY
      201 LATNASREPT PREACHEDPY GPIYNDEEA QIFVSDAGVV AVAFGLYKLA
      251 AAFKWWYR NYAUPLLIV AWLLITYIQ HTHPELPHYD SSEWDWLEGA
      301 LATKRIQGI ENFPRHITL THVAHLFST MPRYRAHEAT KAIRPILGQY
```

301 YHSDTIYAF AWREAGEGI YVEPELERSV FWNKKK

HITS AT: 111-111, 14-111, 111-126

MF Unspecified

CI MAN

SE CA

IC STM Files: CA, CAPIUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPIUS (1967 TO DATE)

REFERENCE 1: 1.1:1040

106 ANSWER 10 OF 36 REGISTRY COPYRIGHT 1997 ACS

EN 158283-28-4 REGISTRY

CN Desaturase, oleyl desaturase A (cytochrome clone pSF1-165F reduced)

reduced, PCL (CA INDEX NAME)

OTHER NAMES:

CN Desat.-11 Fatty acid desaturase (Glycine max clone pSF1-165K)

ES PROTEIN SEQUENCE

SQL 379

```
SEQ      1 MGAGSEMAEK EYQGHFIEF VNTTHPEPTV GQIKKAIPPH CQPFSLIIF
      51 SYFYDLEFA FIFTIATTYF HLLQFFSLI AWPLYWVLOQ CLLIGVWVIA
     101 HEDGSHAFSP YQWVDVDEL THSTILVVEY FSWHSHREH HSNTGSLERD
      151 EYFVETKTSY VAWKAPYINN PLGAASLLV TLTGWMKYL AFNVSGREYD
      201 SPASHYHNYA FIYNDEELI IYVDVALES VYSLYEVAT LKGLVWLLCV
      251 YGPIILLNG FIVTITYLQH THFALFHYDS SEWDWLECAL ATNRLYGIL
      301 NTHPRHITIT THVAHLFSTI THVAHEATIN ALPILGEYV QEDDTFYFA
```

301 LWRKAFEDIT YHEEGCTEP QVWYRNKY

HITS AT: 101-101, 101-111, 111-115

MF Unspecified

CI MAN

SE CA

IC STM Files: CA, CAPIUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPIUS (1967 TO DATE)

REFERENCE 1: 1.1:1040

106 ANSWER 20 OF 36 REGISTRY COPYRIGHT 1997 ACS

EN 158283-26-2 REGISTRY

CN Desaturase, oleyl desaturase A (Brassica napus clone pCF2-165D

reduced, PCL (CA INDEX NAME)

OTHER NAMES:

CN Desat.-12 Fatty acid desaturase (Brassica napus clone pCF2-165D)

ES PROTEIN SEQUENCE

SQL 383

```
SEQ      1 MGAGGHILNC PPSKSETON IKR/PCETPP ETGGELEKAI PPHCFYRSIP
      51 RSPSHLIWDI IASCFYYVA TTYFPLLNP LSYFAWLYW ACQGEVLTGV
      101 KATHLEEN FULLER BT/LIBRARY 308-4190
```

```

101 WVIAHECGHA AFSDYQWLED TWGLIFHSFL LVVWFSWYYS HRRHESNTGS
=====
151 LERDEVEVPR ESQTSSTGAS TSTTFGRVM LTVQFTLGWP LYLAENVSGR
201 PVTGGFACHF HKNAPIYNER ERLQIYISDA GILAVCYGLL PYAAVQGVAS
301 MACEFLVPLL IVNGFLVLT YLQETHPSLP HYDSEWIWL EGALATVDRD
401 YGLNLSFHN ITCTEAAHL PSTTHPHYAM EATKAIKFL GEYYQFDGTR
=====

```

401 WVKAMWREAK ECIYVEPDEQ GEEFGVFWYN NEL

HITS AT: 130-133, 141-143, 145-147

MF Unspecified

CI MAN

SE CA

SC STM Files: CA, CAPUS

1 REFERENCED IN FILE CA (1967 TO DATE)

1 REFERENCED IN FILE CAPUS (1967 TO DATE)

REFERENCE 1: 1:1:1664

106 ANSWER 11 OF 36 REGISTRY COPYRIGHT 1967 ACS

BN 158283-24-0 REGISTRY

CM Desaturase, leagl desaturase A (Arabidopsis thaliana clone p92103)  
reduced: (1) (CA INDEX NAME)

OTHER NAMES:

CM Delta-12 fatty acid desaturase (Arabidopsis thaliana clone p92103)

CM Oleate desaturase (Arabidopsis thaliana clone pE2a gene FAD2)

PC PROTEIN SEQUENCE

SQL 383

```

SEQ      1 MGAGGEMVPP TTPKSTET TETPKCKEP EKVGLPWAI EPHCFKESIP
      61 KPSFYLISDI IACQFYVA EHYFSLLPQP EGYLAWPLYW AQCGCVLTGI
101 WVIAHECGHA AFSDYQWLED TWGLIFHSFL LVVWFSWYYS HRRHESNTGS
=====
151 LERDEVEVPR ESQTSSTGAS TSTTFGRVM LTVQFTLGWP LYLAENVSGR
201 PVTGGFACHF HKNAPIYNER ERLQIYISDA GILAVCYGLY PYAAVQGVAS
301 MACEFLVPLL IVNGFLVLT YLQETHPSLP HYDSEWIWL EGALATVDRD
401 YGLNLSFHN ITCTEAAHL PSTTHPHYAM EATKAIKFL GEYYQFDGTR
=====

```

401 WVKAMWREAK ECIYVEPDEQ GEEFGVFWYN NEL

HITS AT: 130-133, 141-143, 145-147

MF Unspecified

CI MAN

SE CA

SC STM Files: CA, CAPUS

1 REFERENCED IN FILE CA (1967 TO DATE)

1 REFERENCED IN FILE CAPUS (1967 TO DATE)

REFERENCE 1: 1:1:1664

REFERENCE 2: 1:1:1498

106 ANSWER 2 OF 36 REGISTRY COPYRIGHT 1967 ACS

BN 156532-36-4 REGISTRY

CM Desaturase, leagl desaturase (Synecoccus strain PCC 7102 gene desA)  
reduced: (1) (CA INDEX NAME)

OTHER NAMES:

CM Delta 12 desaturase (Synecoccus strain PCC 7102)

PC PROTEIN SEQUENCE

SQL 347

```

SEQ      1 HESVTVPESA TTHKHPNL ELALILDTLP EKVYEINPLK AWRVLEVA
      51 ATAGCYALLA IAWYILLIV WELTGTTLTG EFWIGHQGH EFSRQWVN
=====
101 NLVGHLAFLP LIYFESWRI LNNHHHKYTN NMEDNAWAP ETPELYDSE
=====

```

151 AFIKAVYPAI RGFLWWLASV IHQLKLFHFW FAFEGHQREQ VRFSALFVII  
 251 AGAIAFFPME YLIGVWGUVV FWIMPWLSYH FWISTFFLVH HTVPEIPFSY  
 351 RQKWEATAQ LSATVHCDFP KWTEVLCHDI NVHVPHRLST GIPSYNLEKA

=====

351 YASIQUNWGE YVETFEWE IMKAITEQCH LYDAENNYIS FAQHQR

HITS AT: 6-90, 102-10, 123-87

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIB

1 REFERENCES IN FILE CA (1-67 TO DATE)

1 REFERENCES IN FILE CAPLUS (19-7 TO DATE)

REFERENCE 1: 1.0:2-0117

REFERENCE 1: 1.1:24-1

LIFE ANSWER 13 OF 10 REGISTRY COPYRIGHT 1993 ACS

EN 156532-35-3 REGISTRY

CH Desaturase, fatty acid (Synchocystis strain PCC 6714 gene desA reduced) (CC1) (CA INDEX NAME)

OTHER NAMES:

CH Delta 12 desaturase (Synchocystis PCC6714)

EC PROTEIN SEQUENCE

SQL 349

SEQ 1 MTATPPIAP TETSSNPRI IALCLKQDI KTIPEFCFK KASHAWLVL  
 51 ITLGIALCY AGIYLPWYQ LPPWIKWTST ALIGAPVCH DCHRSFAEK

101 RWNNDLCHI APAPLIYER SWELIGHERR DRINKLEVEN AWI PWEVLEAF

151 QASPAIVLE VETATGPWW TGIPIHWGLK RPYLENPAER DRNKVPLSIA

201 VYFIAAAVAE PAKITIGVW GPVDFWLMW LYHFWNSTF TYPHETIHEI

251 RFPDAEPWA ABAQLNGTVH CDFPFWVEVL CHFINVHIFH ELVAIPSYN

=====

301 IGLAHANPQ NWQDFLYPRT FHWGLMQQIS GCHLNIPEN CYETESCK

HITS AT: 6-90, 106-10, 180-90

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIB

1 REFERENCES IN FILE CA (1-67 TO DATE)

1 REFERENCES IN FILE CAPLUS (19-7 TO DATE)

REFERENCE 1: 1.1:24-23

LIFE ANSWER 14 OF 10 REGISTRY COPYRIGHT 1993 ACS

EN 152208-02-1 REGISTRY

CH Desaturase, fatty acid (omega-3 Brassica napus clone BNS gene fad3 reduced) (CC1) (CA INDEX NAME)

OTHER NAMES:

CH omega-3 fatty acid desaturase (Brassica napus clone BNS gene fad3)

EC PROTEIN SEQUENCE

SQL 377

SEQ 1 MVAVDQSN ANDQRENPQ AQDFKIGDI EAGLPEKCV ELPLREMEYV  
 51 ADIFATNAL AVAAVYEDSW FFWPLWAAQ GTLPWALFVL CHICGRGFES

101 DIFLUNIAQ HILDSFILVP YRQWIKSHET RQNRCHVEN LEXWVILPEK

151 IYENLSHETP HLENTPLPH LATPLYLWYR SPKECKHYN EYCSLEPASE

201 RRLIATNED WSIMLATVY LDFLVGPVTV LEYGVFYII FVMWLDVNTY

251 LHHGHGKRL PWYRGKWSY LRGGLTTIDE DYGFNNIEH DIGTHVILHL

=====

KATHLEEN FULLER BT.LIBRARY 308-4290

351 FDQIPHYHLV DATHSAKHVL GRYYREPKTS GAIPHVLVES LVASIKKDHY  
 351 VDETSDVEFY ETDPDFLYVYA SDKSKIN

HITS AT: 91-96, 123-135, 251-256, 295-299

MF Unspecified

CI MAN

SE CA

LC STN Files: CA, CAPLUS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 12:47:48

1.6 ANSWER 15 F 15 REGISTRY COPYRIGHT 1992 ACS

RI 152208-01-0 REGISTRY

CI Desaturase, fatty acid .omega.3- (Brassica napus chloroplast-encoded  
 clone BND gene-fact precursor reduced) (NCI) (CA INDEX NAME)

OTHER NAMES:

CI .omega.-3 fatty acid desaturase (Brassica napus chloroplast clone  
 BND gene-fact precursor)

SE PROTEIN SEQUENCE

DEL 329

SEQ 1 MNYCEBIAL VPALAGWAV LNNWLAWPLY WIAQGTMFVA LFLVGHICGH

=====

11 GPECKHREN JVGCHLSEF ILVPYHGMET SRATHERQNHG HVENDESWHP

=====

111 MERNIYRND ETRFFETPL PLTILAYPFY LWAESEKNG SHYEPDSDF

111 LKPEKNVIT STACTAHAV LLVCLNEVNG PMQMLKLYVI PYWINVMWLD

111 ETVYHNNH ESKLWYRGK EWVTLGGIT TLDSDYCLIN NTHHDICHTV

=====

111 IHHLEQNH TRINEATWAA KEVLGKYRE PDKSGPLPLH LGLILANSIK

===

111 EDEPUSIED VVYVEADNL YGHIEVTAE

HITS AT: 46-50, 51-55, 116-117, 242-253

MF Unspecified

CI MAN

SE CA

LC STN Files: CA, CAPLUS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 12:47:48

1.6 ANSWER 16 F 16 REGISTRY COPYRIGHT 1992 ACS

RI 149956-03-6 REGISTRY

CI Desaturase, fatty acid .DELTA.11- Arabidopsis thaliana clone  
 pFadx-2 fragment reduced (NCI) (CA INDEX NAME)

OTHER NAMES:

CI .DELTA.11-desaturase fragment Arabidopsis thaliana clone pFadx-2  
 cistid

SE PROTEIN SEQUENCE

DEL 156

SEQ 1 LTYVRAFTN WAINVATPL TLQMPSEDR ERFDFGAPP FNLADIFAAI

11 EHCWVENFW MMLYVURDV AIVFGLAAVA AYENNWLWLP LYWFAQGTMF

101 WAILVLDHDC SHGSFSNDF LNSVAGHLH SSILVPYHGW RISHETHEQN

== ==

=====

101 HGHVEN

=

HITS AT: 103-112, 144-151

MF Unspecified

CI MAN

SE CA

LC STN Files: CA, CAPLUS, TOXLIT

KATHLEEN FULLER BT/LIBRARY 308-4290



1 REFERENCES IN FILE CA (1967 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 119:153376

126 ANSWER 27 OF 36 REGISTRY COPYRIGHT 1967 ACS

EN 149956-02-5 REGISTRY

EN Desaturase, fatty acid .DELTA.15- (corn clone pPCR20 fragment reduced (901) (CA INDEX NAME)

OTHER NAMES:

EN .DELTA.-15 desaturase fragment (Zea mays clone pPCR10)

EV PROTEIN SEQUENCE

SQL 126

SEQ 1 HHHQNHSHIR DESWHFITEK LYEQLEPRTE KLEFTTFEEL LAEPVYLLYE

=====

51 SPCKLSHFEL PSSDLFSFKE KSDVMNSTTC WCIMLASLLA MACAFGPLQV  
101 LKMGIEIYLV EFWIDENY LRRHGH  
=====

HITS AT: 1-3, 122-126

MF Unspecified

CI MAN

SE CA

IC STN Files: CA, CAPLUS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 119:153376

126 ANSWER 28 OF 36 REGISTRY COPYRIGHT 1967 ACS

EN 149956-01-4 REGISTRY

EN Desaturase, fatty acid .DELTA.15- (soybean clone pSFD-118bwp reduced (901) (CA INDEX NAME)

OTHER NAMES:

EN .DELTA.-15 desaturase (Glycine max clone pSFD-118bwp plastid)

EN .omega.-3 fatty acid desaturase (Glycine max chloroplast clone GMD gene fad1)

EV PROTEIN SEQUENCE

SQL 453

SEQ 1 MATWYHQKQG LKILAPVIEP PEGGAALSST GENEFEETNE VVAGPKFQPL

51 RCHLREFNMG LKTSAPLVA FIEEBQKSTG LTINGTNGVER EHLPEFDPGA  
101 PPSFNLADIE AATPHRCUVE DEWRSMSTYV EDVIAVEGLA AAAYINNWL  
151 VWFLYWAAQD TMEWALEYIC HDGCHQSENI NSELNQVVGH LIESSILVPY  
=====

201 HGWRKSHETE HQHGHAFND ESWHPLPEKI EFLDQVTEN LEFTAPPELL  
=====

251 ASFVYLFERS EGTGSHFDE SSDLFVPNER EDVITSTACW AAMLGLLVGL

301 GFTGPIQLL KLYGVYVIEF VMWLDLVYL HENGHEKLP WYRGKWSYL  
=====

351 RGHITIEDD YGWINNIHED LGTHVIHHLF EQIPHYELVE ATEAAKPVFG  
=====

401 KYKREPPFSA APLPFELIGE LIESFETDHF VSDTGDVVYY QTDSKINGSS

451 KLE

HITS AT: 171-175, 207-214, 301-335, 374-378

MF Unspecified

CI MAN

SE CA

IC STN Files: CA, CAPLUS, TOXLIT

2 REFERENCES IN FILE CA (1967 TO DATE)

2 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 120:47048

REFERENCE 2: 119:153-76

126 ANSWER 29 OF 36 REGISTRY COPYRIGHT 1987 ACS

EN 149956-00-3 REGISTRY

CU Desaturase, fatty acid DELTA.15- soybean clone pXF1 reduced) (9CI)  
(CA INDEX NAME)

OTHER NAMES:

CU DELTA.15 desaturase (Glycine max clone pXF1 microsomal)

CU Omega-3 fatty acid desaturase (Glycine max clone GM3 gene fad3)

EC PROTEIN SEQUENCE

SQL 380

SEQ 1 NNTHTTAY AANNQYQNG SSEDEDFCAP PPFKIAEIPA SIPYHCWVKH  
11 FWRSLSTYLR DVNIAALVA AAIEFIMWIL WLIYCFIQGT MPWALFVLGH

111 DCHGSDPDS PLNSINQHI LESSIANPYE GWEISHFTHH QHGHIEKDE

111 SWNFTETNRY EINDSMALI FETVPEPLPV YPIYLFSESP GREGSHFNRY

111 SILSTPEERK GIALSTLWA TNEFLHLYLS FITSPLLVLK LYGIPYWIFV

111 MWLFSTYLR ESHRQKLPW YEGKRWYIR GGLITVIRRY GRIYNIHEDI

111 GCHVHHLEP QTERYHREA TQAAPNLDL YTEPEFSAP LPEHLIKYLI

111 QNIPQDHYE MDSQYVQT ISLLIESQED

HITS AT: 130-134, 136-143, 161-165, 163-80

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

REFERENCES IN FILE CA (1967 TO DATE)

REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 119:147048

REFERENCE 1: 119:153-76

126 ANSWER 30 OF 36 REGISTRY COPYRIGHT 1987 ACS

EN 149955-99-7 REGISTRY

CU Desaturase, fatty acid DELTA.15- Brassica napus clone pNSFd-2  
C-terminal fragment reduced: (9CI) (CA INDEX NAME)

OTHER NAMES:

CU DELTA.15 glycerolipid desaturase Brassica napus clone pNSFd-2  
plantier

EC PROTEIN SEQUENCE

SQL 404

SEQ 1 PPFQSDNRP EFLNSHAWA INVTHPTD SEUSEPIEEE PHTQRFDPGA

11 PPFENALIR AAIPEHCWVE NWKSMYVW RELATFALA AGAAYLINWL

111 MWPLTWIAPG THFWALFPLS HOGSHRDEIN DEELNCVCH LHRSSILAPY

111 GWEISHFTH EQNHSQVEND ESWHETNENI YELDEPTEF EKFTLPIVML

111 AYPEYMAES PGEKGSHTHE EDLFLPHEE NDULTSTACW TAMAVLINCL

111 DFTNQHQLL KLVVTPWIS MWLDFVTL EHRGHEDELP WYRKREWSYL

111 EGGLTIEDD YGLNNINHD GCHVHHLEP PDIPYHAE ATEAAKPVLG

111 HYKEPDESS PLPLHLMHIL AKSIKEDHYV SDEGDIVVYE ADPNLYGEIK

111 VTAE

HITS AT: 121-125, 157-164, 181-185, 324-328

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

KATHLEEN FULLER BT/LIBRARY 308-4200

1 REFERENCES IN FILE CA (1967 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 119:153246

126 ANSWER 31 OF 36 REGISTRY COPYRIGHT 1987 ACS

EN 149955-98-6 REGISTRY

CU Desaturase, fatty acid DELTA-11- (Brassica napus clone pPNSF3-f2  
C-terminal fragment reduced) (P1) (CA INDEX NAME)

OTHER NAMES:

CU DELTA-11 glycerolipid desaturase (Brassica napus clone pPNSF3-2  
microsome)

EN PROTEIN SEQUENCE

SQL 378

SEQ 1 LTVVSSSSPP DEEPKQRE DEGAAPPPHL ADIRAAIPKH CWVKNPWKSH  
51 LTVVDELAIN PALAAGAYAL NWLVWPLYW LAQGTWAL FVLGHDCGEG

101 LENVLPBAND VVHLLHSLI LVVYRWRLS HFTHHQNHCH VENDESWEHM

151 LELVYKSLDK PTEFFRFTLP LVHLYPPYL WARSFGFKGS HYHEDSELFL

161 PFEEDNLTS CANTANAL LVCLNFVSGP HQLFLYVIP YWINVMWLDL

181 LTVLHHHHE DKLWYHRE WYLLGGTLT LFDYGLINN EHHDGTHV

201 HHLFFQIRSY HNEATEAAK LVLSHYREP DQGLDELHL LGILAKSIF

251 DFNDEEDCV VVEADENIN GHVNTAE

HITS AT: 9-42, 111-114, 151-158, 193-202

MF Unspecified

CI MAN

SA CA

SC STM Files: CA, CAPLUS, TOXLET

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 119:153246

126 ANSWER 32 OF 36 REGISTRY COPYRIGHT 1987 ACS

EN 149955-97-5 REGISTRY

CU Desaturase, fatty acid DELTA-11- (Arabidopsis thaliana clone  
pACF2-1 reduced) (P1) (CA INDEX NAME)

OTHER NAMES:

CU DELTA-11 fatty acid desaturase (Arabidopsis thaliana clone pACF2-2  
plastid)

CU Omega-3 fatty acid desaturase Arabidopsis thaliana chloroplast  
clone (P1) (reduced precursor)

CU Omega-3-Fatty acid desaturase Arabidopsis thaliana clone g45)

EN PROTEIN SEQUENCE

SQL 446

SEQ 1 HANENLSEDE LPLPRTYTT HENNELSLIN HEPSESSSS YKISSSPLSF

51 GLNEDGSTR NWALNSSL LTVFEECHL EELNQRFP GAFFPENLAD

101 IRALPHEW VHPWESLKY VVEVAIVFA LAAGAAYLNN WLVWPLYWLA

151 QGTWALWLV LADDOCHCF SDIKLNSTV GHLDSSILV DYHWRISER

201 PHQREGHVY NGENWHHCE HUNTLDEPT REFRSTLPLV HLAYPPYLWA

251 RSDGFKGSHY HEDDLFLPK EELVLTSTA CWTANALLV CLNETIGPIQ

301 HLELYGIPYW LNMWLDFTV VHHHSHEOK LKYYKEWS YLGGTLTLO

351 RDYGLINNIH HDGTHVIRH LPPVLPYHL VEATEAAKPV LGKYYREPDK

401 SGLPLHLLE ILAKSIEDH YUSDEGEVY YEDPNLYGE WKVREAD

HITS AT: 165-167, 199-206, 323-327, 366-370

KATHLEEN FULLER BT/LIBRARY 306-4290

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

4 REFERENCES IN FILE CA (1967 TO DATE)

4 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 101:297499

REFERENCE 2: 100:184029

REFERENCE 3: 100:47098

REFERENCE 4: 109:133376

1.6 ANSWER 33 OF 36 REGISTRY COPYRIGHT 1997 ACS

EN 149955-96-4 REGISTERED

CN Desaturase, fatty acid DELTA.15- (Arabidopsis thaliana clone pCF3 reduced) (OCI) (CA INDEX NAME)

OTHER NAMES:

CN DELTA.15-desaturase (Arabidopsis thaliana clone pCF3)

CN Omega-3 fatty acid desaturase (Arabidopsis thaliana clone CF3 gene fa13)

FS PROTEIN SEQUENCE

SQL 386

SEQ 1 MIVAMDDQSTN VNELEGACIE EKEERFDRIA QPPEKIGDIR AAIPKHQWVK

51 SPSRDMYYTV EDIAVAZALA IAAVYVDSWF LWFYWAACQ TLFWAIFVLG

101 HQCGHGFEDD LIDMSVVGH ILSFILVPY HGRERISERTH QNHGHVEND

=====

151 EKWVPLEEN YKLEHSTEM LEYTVLEPHL AYELYLCYFS PEKEGSHENP

101 YTSLPASSER ELIATSTTOW LIMEVLIAL SEYEGPLAVI KVGVPYIIF

151 VWELIATYTL HSHCHIEPLF WYRGKWSYL RGLATIDED YGIFNNIHD

=====

101 IGTHYHHLF EQLHYHIND ATKAAHVLG EYEEPEKTES AIPHLVESL

=====

151 VASIRKDEHY SDTCQIVFYE TDPDLYVYAS DESKIN

HITS AC: 101-103, 107-149, 161-165, 304-308

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

4 REFERENCES IN FILE CA (1967 TO DATE)

4 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 100:47098

REFERENCE 2: 109:133376

1.6 ANSWER 34 OF 36 REGISTRY COPYRIGHT 1997 ACS

EN 148814-49-7 REGISTERED

CN Desaturase, fatty acid DELTA.15- (Brassica napus clone pBNDES3 gene fa13 reduced) (OCI) (CA INDEX NAME)

OTHER NAMES:

CN Omega.3 Lin. late desaturase (Arabidopsis reduced)

FS PROTEIN SEQUENCE

SQL 383

SEQ 1 MIVAMDDQSTN VNEESNARHE EGEDPSAQFP EKIGDIEAAI PEHCWVNSPL

51 RSMSTVTEDL FAVAAAMIAA VYFDSWFLWP LYVVAQSTLF WAIFVLGHDC

101 GHGSEGDIEPL LNSVVGHILH SFILVPYH W RLSHRTTHQN HGHVENDESW

=====

151 VELPEKLYEN LPHSTEMLAY TVPLEMLAYP IYLWYRSPGE EGSFENPYSS

KATHLEEN FULLER BT/LIBRARY 308-4290

201 LEAPSEPKLI ATSTTCWSIM LATLVYLSFL VDPVTVLKVY GVPYIIFVMW  
201 LDVAVYLLHHH GHLEKLPWYP GKWSYLRGG LPTTLELYGI FNNIHHDIGT

201 HVVHLETPQI PHVHLVLAIF AAPHVLGEMY REPKTSCAIP IHLVESLVS

201 IKPTHYVSET GDVIFYETEE DLYVYASDEFS KIN

HITS AT: 98-140, 124-141, 158-262, 301-305

MF Unspecified

CI MAN

CF CA

LC STN Files: CA, CALUS, TOKKIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CALUS (1967 TO DATE)

REFERENCE 1: 121:97339

REFERENCE 2: 119:31620

126 ANSWER 34 OF 36 REGISTRY COPYRIGHT 1997 ACS

RI 148734-39-8 REGISTRY

CI Desaturase, linoleate (Synchocystis strain PCC 6803 clone csy75-3.5 reduced) (CA INDEX NAME)

OTHER NAMES:

CI DELTA-6-Desaturase (Synchocystis clone pSy75-3.5)

CI Desaturase, linoleate (Synchocystis strain PCC 6803)

CI GenBank 100-014-derived protein (U16-358)

CI Protein (Synchocystis strain PCC 6803 clone csy75-3.5) open reading frame s110262 reduced

FI PROTEIN SEQUENCE

QQL 359

SEQ 1 MDAARKEPT PDEGRAVIN QMDVYFAEH GLTQRDNPSM YLKTLLIIVLW

21 LDFAMAFVLF AFVIFVRLI QCIDLAIALA AFSENUGHDA NENAYSSNPH

201 LNNVLSHTNY EYHLSFELWR YENNYLHHTY TNLGHDVEI HGDGAVEMSP

201 EQPHUSIYRF QQSYIWCIAL PIPFYWELYD VYLVNLKGGY HDHKIPPFQF

201 LKIAALLGK LKLGYPGL PLALGFSIPE VLIGASVTYM TNGIVVCTIF

201 LKIAVLESTE PLIPDGLGGA LKDMAICDL RTTANPATNN PFWNWFCGSL

201 NBLVTHLEFP NI THIRNPQL ENIKDVCE FQVEYKVYPT FKAALASNYR

201 WKEALGERS

HITS AT: 88-01, 123-124, 302-303

MF Unspecified

CI MAN

CF CA

LC STN Files: CA, CALUS, TOKKIT, USPATEULL

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CALUS (1967 TO DATE)

REFERENCE 1: 126:31906

REFERENCE 2: 126:70918

REFERENCE 3: 119:154315

REFERENCE 4: 119:64918

126 ANSWER 35 OF 36 REGISTRY COPYRIGHT 1997 ACS

RI 131198-85-1 REGISTRY

CI Desaturase, acyl coenzyme A (Saccharomyces cerevisiae reduced) (9C1) (CA INDEX NAME)

FS PROTEIN SEQUENCE

• SQL 510

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SEQ      1 MPTSGTTIEL IDQQFPKDDG ASSGIVDEVD LTEANILATG LNKKAPRIVN
      51 GFGGILMGSKK MVSVEFDFKKG NKKKSNLLDL LEPDNQEKKEE AKTKIHISEQ
     101 PWTLLNNWHQH LNWLNMMVIVC GMPHIGWYFA LGGKVPLHLN VFLPSVEFYA
     151 VGGVSTAGY HRLWSEHSYS AHWPLRLFYA LFGCASVEGS AKWWGHSHEI
      ===
     201 HHRNTDTLRD PYDAREGLWY SHMGWMLLFP NPFYKAFADI TDMTDLWTIR
      ===
     251 FQHFHYILLM LLTASVLPFL ICGYFENDYM GGLIYAGFIR VFVLCQATEC
     301 INSMARYIST QPFDFKRTFF DNWITAIVTF GEGYNEFHEE FPTDYENAIK
      =====
     351 WYQYDPTKVI IYLTSLVGLA YDLKKFSQIA LFWALIQQEQ KKINKKKAKI
     401 NWSIVLTDLP MWDEQTFIAM SKENKGLVII SGIVHDVSGY ISEHFGGETL
     451 IKPALGPDAT KAFSGGVYRH SNAAQNVIAL MRCVAVIFESH NSAIEMASKE
     501 GEIYETGFFF

```

HITS AT: 195-204, 335-339

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 114:18574